

WEST Search History

[Hide Items](#)[Restore](#)[Clear](#)[Cancel](#)

DATE: Saturday, September 24, 2005

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
		<i>DB=USPT; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L1	6294662.pn.	1
<input type="checkbox"/>	L2	6683156.pn.	1
<input type="checkbox"/>	L3	6649588.pn. or 6428966.pn. or 6294662.pn. or 5916751.pn.	4
<input type="checkbox"/>	L4	Tabibzadeh.in.	7

END OF SEARCH HISTORY

WEST Search History

DATE: Saturday, September 24, 2005

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
	<i>DB=USPT; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L1	5874479.pn.	1
<input type="checkbox"/>	L2	tgf\$ same (type4 or type-4 or (type near 4))	15
<input type="checkbox"/>	L3	(lefty1 or lefty2 or lefty-1 or lefty-2 or leftyb or lefty-b or leftya or lefty-a) and protein	6
<input type="checkbox"/>	L4	(stra3 or stra-3) and protein	13
	<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L5	(lefty1 or lefty2 or lefty-1 or lefty-2 or leftyb or lefty-b or leftya or lefty-a) and protein	18
<input type="checkbox"/>	L6	L5 not l3	12
<input type="checkbox"/>	L7	L5 not l3	12
<input type="checkbox"/>	L8	(stra3 or stra-3) and protein	96
<input type="checkbox"/>	L9	(stra3 or stra-3) same (protein or polypeptide or peptide)	95
<input type="checkbox"/>	L10	transforming near growth near factor near beta near 4	74
<input type="checkbox"/>	L11	L10 not l2	74
<input type="checkbox"/>	L12	L11 not l3	74
<input type="checkbox"/>	L13	L12 not l5	74

END OF SEARCH HISTORY

Trying 31060000009999...Open

DIALOG INFORMATION SERVICES

PLEASE LOGIN:

***** HHHHHHHH SSSSSSSS? ### Status: Signing onto Dialog *****

ENTER PASSWORD:

***** HHHHHHHH SSSSSSSS? *****

Status: Login successfulWelcome to DIALOG

Dialog level 05.06.01D

Last logoff: 21sep05 09:05:16

Logon file405 26sep05 07:14:32

*** ANNOUNCEMENT ***

--UPDATED: Important Notice to Freelance Authors--

See HELP FREELANCE for more information

NEW FILES RELEASED

***Computer and Information Systems Abstracts (File 56)

***Electronics and Communicationss Abstracts (File 57)

***Solid State and Superconductivity Abstracts (File 68)

***ANTE: Abstracts in New Technologies (File 60)

***Civil Engineering Abstracts (File 61)

***Aluminium Industry Abstracts (File 33)

***Ceramic Abstracts/World Ceramic Abstracts (File 335)

***CSA Life Sciences Abstracts (File 24)

***Corrosion Abstracts (File 46)

***Materials Business File (File 269)

***Engineered Materials Abstracts (File 293)

***CSA Aerospace & High Technology Database (File 108)

***CSA Technology Research Database (File 23)

***METADEX(r) (File 32)

***FDAnews (File 182)

***German Patents Fulltext (File 324)

RESUMED UPDATING

***Canadian Business and Current Affairs (262)

***CorpTech (559)

Chemical Structure Searching now available in Prous Science Drugs
of the Future (F453), IMS R&D Focus (F445), Beilstein Facts (F390),
and Derwent Chemistry Resource (F355).

>>> Enter BEGIN HOMEBASE for Dialog Announcements <<<

>>> of new databases, price changes, etc. <<<

* * *

SYSTEM:HOME

Cost is in DialUnits

Menu System II: D2 version 1.7.9 term=ASCII

*** DIALOG HOMEBASE(SM) Main Menu ***

Information:

1. Announcements (new files, reloads, etc.)
2. Database, Rates, & Command Descriptions
3. Help in Choosing Databases for Your Topic
4. Customer Services (telephone assistance, training, seminars, etc.)
5. Product Descriptions

Connections:

6. DIALOG(R) Document Delivery
7. Data Star(R)

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/H = Help /L = Logoff /NOMENU = Command Mode

Enter an option number to view information or to connect to an online service. Enter a BEGIN command plus a file number to search a database (e.g., B1 for ERIC).

? b 155 medicine

Terminal set to DLINK

*** DIALOG HOMEBASE(SM) Main Menu ***

Information:

1. Announcements (new files, reloads, etc.)
2. Database, Rates, & Command Descriptions
3. Help in Choosing Databases for Your Topic
4. Customer Services (telephone assistance, training, seminars, etc.)
5. Product Descriptions

Connections:

6. DIALOG(R) Document Delivery
7. Data Star(R)

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/H = Help /L = Logoff /NOMENU = Command Mode

Enter an option number to view information or to connect to an online service. Enter a BEGIN command plus a file number to search a database (e.g., B1 for ERIC).

? e transforming growth factor beta

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26sep05 07:14:34 User228206 Session D2511.1
      $0.00      0.211 DialUnits FileHomeBase
$0.00 Estimated cost FileHomeBase
$0.00 Estimated cost this search
$0.00 Estimated total session cost      0.211 DialUnits

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SYSTEM:OS - DIALOG OneSearch

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File 155:MEDLINE(R) 1951-2005/Sep 26
      (c) format only 2005 Dialog
File 5:Biosis Previews(R) 1969-2005/Sep W3
      (c) 2005 BIOSIS
File 34:SciSearch(R) Cited Ref Sci 1990-2005/Sep W3
      (c) 2005 Inst for Sci Info
File 35:Dissertation Abs Online 1861-2005/Aug
      (c) 2005 ProQuest Info&Learning
File 48:SPORTDiscus 1962-2005/Apr
      (c) 2005 Sport Information Resource Centre
File 65:Inside Conferences 1993-2005/Sep W3
      (c) 2005 BLDSC all rts. reserv.
File 71:ELSEVIER BIOBASE 1994-2005/Sep W3
      (c) 2005 Elsevier Science B.V.
File 73:EMBASE 1974-2005/Sep 26
      (c) 2005 Elsevier Science B.V.
File 91:MANTIS(TM) 1880-2005/Jun

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2001 (c) Action Potential
 File 94:JICST-EPlus 1985-2005/Jul W5
 (c) 2005 Japan Science and Tech Corp (JST)
 File 98:General Sci Abs/Full-Text 1984-2004/Dec
 (c) 2005 The HW Wilson Co.
 File 135:NewsRx Weekly Reports 1995-2005/Sep W3
 (c) 2005 NewsRx
***File 135: New newsletters are now added. See Help News135 for the complete list of newsletters.**
 File 144:Pascal 1973-2005/Sep W3
 (c) 2005 INIST/CNRS
 File 149:TGG Health&Wellness DB(SM) 1976-2005/Sep W3
 (c) 2005 The Gale Group
 File 156:ToxFile 1965-2005/Sep W4
 (c) format only 2005 Dialog
 File 159:Cancerlit 1975-2002/Oct
 (c) format only 2002 Dialog
***File 159: Cancerlit is no longer updating.**
 Please see HELP NEWS159.
 File 162:Global Health 1983-2005/Aug
 (c) 2005 CAB International
 File 164:Allied & Complementary Medicine 1984-2005/Sep
 (c) 2005 BLHCIS
 File 172:EMBASE Alert 2005/Sep 26
 (c) 2005 Elsevier Science B.V.
 File 266:FEDRIP 2005/Jun
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 File 369:New Scientist 1994-2005/Jun W4
 (c) 2005 Reed Business Information Ltd.
 File 370:Science 1996-1999/Jul W3
 (c) 1999 AAAS
***File 370: This file is closed (no updates). Use File 47 for more current information.**
 File 399:CA SEARCH(R) 1967-2005/UD=14313
 (c) 2005 American Chemical Society
***File 399: Use is subject to the terms of your user/customer agreement.**
 Alert feature enhanced for multiple files, etc. See HELP ALERT.
 File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
 (c) 1998 Inst for Sci Info
 File 444:New England Journal of Med. 1985-2005/Sep W2
 (c) 2005 Mass. Med. Soc.
 File 467:ExtraMED(tm) 2000/Dec
 (c) 2001 Informania Ltd.
***File 467: F467 no longer updates; see Help News467.**

7.

Set Items Description
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Ref	Items	RT	Index-term
E1	2		TRANSFORMING GROWTH FACTOR B-1
E2	1		TRANSFORMING GROWTH FACTOR B-1 TGF-B1
E3	62977	39	*TRANSFORMING GROWTH FACTOR BETA
E4	1		TRANSFORMING GROWTH FACTOR BETA (TGF-BETA)
E5	1		TRANSFORMING GROWTH FACTOR BETA (TAFB)
E6	7		TRANSFORMING GROWTH FACTOR BETA (TGF BETA)
E7	1		TRANSFORMING GROWTH FACTOR BETA (TGF) -BETA(1)
E8	1		TRANSFORMING GROWTH FACTOR BETA (TGF- BETA)
E9	47		TRANSFORMING GROWTH FACTOR BETA (TGF-BETA)
E10	1		TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) AND
E11	2		TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) REC

E12 4 TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) SUP

Enter P or PAGE for more

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Ref	Items	Type	RT	Index-term
R1	57199		39	*TRANSFORMING GROWTH FACTOR BETA
R2	3518	U	2	TGF BETA
R3	25165	X		DC=D11.303.553.992.720.
R4	14733	X		DC=D11.303.900.720.
R5	25165	X		DC=D12.644.276.984.720.
R6	14733	X		DC=D12.644.900.720.
R7	39898	X		DC=D24.185.348.900.720.
R8	278463			DC=D24.35.190
R9	130149			DC=D24.35.540.360
R10	39898	X		DC=D24.611.350.400.800.
R11	0	X	3	BONE-DERIVED TRANSFORMING GROWTH FACTOR
R12	0	X	3	PLATELET TRANSFORMING GROWTH FACTOR

Enter P or PAGE for more

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Ref	Items	Type	RT	Index-term
R13	8	X	3	TGF-BETA
R14	43232	B	352	GROWTH SUBSTANCES
R15	3919	B	21	TRANSFORMING GROWTH FACTORS
R16	130149			DC=D29.25.540.360
R17	278463			DC=D4.680.190
R18	130149			DC=D4.680.360
R19	120579	B	266	CYTOKINE
R20	19791	B	153	GROWTH FACTOR
R21	0	S	1	BETA TRANSFORMING GROWTH FACTOR
R22	0	S	1	PLATELET DERIVED TRANSFORMING GROWTH FACTOR BE
R23	0	S	1	TRANSFORMING GROWTH FACTOR TYPE BETA
R24	0	S	1	TYPE BETA TRANSFORMING GROWTH FACTOR

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>>>Related terms display completed...

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Ref	Items	RT	Index-term
E1	1		TRANSFORMING GROWTH FACTOR ANTISENSE MESSENGER
E2	1		TRANSFORMING GROWTH FACTOR AUTOCRINE GROWTH FA
E3	12		*TRANSFORMING GROWTH FACTOR B
E4	1		TRANSFORMING GROWTH FACTOR B (TGF-BETA) SOLUBL
E5	1		TRANSFORMING GROWTH FACTOR B IODODEOXYURIDINE
E6	1		TRANSFORMING GROWTH FACTOR B- SUPERFAMILY
E7	1		TRANSFORMING GROWTH FACTOR B-BETA
E8	2		TRANSFORMING GROWTH FACTOR B-1
E9	1		TRANSFORMING GROWTH FACTOR B-1 TGF-B1
E10	62977	39	TRANSFORMING GROWTH FACTOR BETA
E11	1		TRANSFORMING GROWTH FACTOR BETA (TGF-BETA)
E12	1		TRANSFORMING GROWTH FACTOR BETA (TAFB)

Enter P or PAGE for more

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Ref	Items	Index-term
E13	7	TRANSFORMING GROWTH FACTOR BETA (TGF BETA)
E14	1	TRANSFORMING GROWTH FACTOR BETA (TGF) -BETA(1)
E15	1	TRANSFORMING GROWTH FACTOR BETA (TGF- BETA)

E16	47	TRANSFORMING GROWTH FACTOR BETA (TGF-BETA)
E17	1	TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) AND
E18	2	TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) REC
E19	4	TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) SUP
E20	1	TRANSFORMING GROWTH FACTOR BETA (TGF-P) AND PR
E21	1	TRANSFORMING GROWTH FACTOR BETA (TGF-P) SOLUBL
E22	5	TRANSFORMING GROWTH FACTOR BETA (TGFBETA)
E23	1	TRANSFORMING GROWTH FACTOR BETA (TGFBETA1)
E24	612	TRANSFORMING GROWTH FACTOR BETA --ADMINISTRATI

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Ref	Items	Index-term
E25	8	TRANSFORMING GROWTH FACTOR BETA --ADVERSE DRUG
E26	66	TRANSFORMING GROWTH FACTOR BETA --ADVERSE EFPE
E27	21	TRANSFORMING GROWTH FACTOR BETA --AGONISTS --A
E28	2318	TRANSFORMING GROWTH FACTOR BETA --ANALYSIS --A
E29	1290	TRANSFORMING GROWTH FACTOR BETA --ANTAGONISTS
E30	4167	TRANSFORMING GROWTH FACTOR BETA --BIOSYNTHESIS
E31	1298	TRANSFORMING GROWTH FACTOR BETA --BLOOD --BL
E32	3	TRANSFORMING GROWTH FACTOR BETA --BUCCAL DRUG
E33	80	TRANSFORMING GROWTH FACTOR BETA --CEREBROSPINA
E34	2	TRANSFORMING GROWTH FACTOR BETA --CHEMICAL SYN
E35	569	TRANSFORMING GROWTH FACTOR BETA --CHEMISTRY --
E36	92	TRANSFORMING GROWTH FACTOR BETA --CLASSIFICATI

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Ref	Items	Index-term
E37	23	TRANSFORMING GROWTH FACTOR BETA --CLINICAL TRI
E38	144	TRANSFORMING GROWTH FACTOR BETA --DEFICIENCY -
E39	9	TRANSFORMING GROWTH FACTOR BETA --DIAGNOSTIC U
E40	15	TRANSFORMING GROWTH FACTOR BETA --DRUG ADMINIS
E41	22	TRANSFORMING GROWTH FACTOR BETA --DRUG ANALYSI
E42	198	TRANSFORMING GROWTH FACTOR BETA --DRUG COMBINA
E43	237	TRANSFORMING GROWTH FACTOR BETA --DRUG COMPARI
E44	13	TRANSFORMING GROWTH FACTOR BETA --DRUG CONCENT
E45	102	TRANSFORMING GROWTH FACTOR BETA --DRUG DEVELOP
E46	175	TRANSFORMING GROWTH FACTOR BETA --DRUG DOSE --
E47	402	TRANSFORMING GROWTH FACTOR BETA --DRUG EFFECTS
E48	105	TRANSFORMING GROWTH FACTOR BETA --DRUG INTERAC

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Ref	Items	Index-term
E49	272	TRANSFORMING GROWTH FACTOR BETA --DRUG THERAPY
E50	25	TRANSFORMING GROWTH FACTOR BETA --DRUG TOXICIT

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Ref	Items	Index-term
E1	25	TRANSFORMING GROWTH FACTOR BETA --DRUG TOXICIT
E2	9023	TRANSFORMING GROWTH FACTOR BETA --ENDOGENOUS C
E3	8384	TRANSFORMING GROWTH FACTOR BETA --GENETICS --G
E4	2	TRANSFORMING GROWTH FACTOR BETA --HISTORY --HI
E5	1771	TRANSFORMING GROWTH FACTOR BETA --IMMUNOLOGY -
E6	1	TRANSFORMING GROWTH FACTOR BETA --INTRAARTERIA
E7	5	TRANSFORMING GROWTH FACTOR BETA --INTRAARTICUL
E8	1	TRANSFORMING GROWTH FACTOR BETA --INTRACARDIAC

E9	1	TRANSFORMING GROWTH FACTOR BETA --INTRACAVERNO
E10	4	TRANSFORMING GROWTH FACTOR BETA --INTRACEREBRA
E11	1	TRANSFORMING GROWTH FACTOR BETA --INTRACEREBRO
E12	1	TRANSFORMING GROWTH FACTOR BETA --INTRACISTERN

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Ref	Items	Index-term
E13	1	TRANSFORMING GROWTH FACTOR BETA --INTRADERMAL
E14	1	TRANSFORMING GROWTH FACTOR BETA --INTRAGASTRIC
E15	6	TRANSFORMING GROWTH FACTOR BETA --INTRAMUSCULA
E16	5	TRANSFORMING GROWTH FACTOR BETA --INTRANASAL D
E17	1	TRANSFORMING GROWTH FACTOR BETA --INTRAOCULAR
E18	4	TRANSFORMING GROWTH FACTOR BETA --INTRAPERITON
E19	2	TRANSFORMING GROWTH FACTOR BETA --INTRAPLEURAL
E20	5	TRANSFORMING GROWTH FACTOR BETA --INTRAVENOUS
E21	197	TRANSFORMING GROWTH FACTOR BETA --ISOLATION AN
E22	9153	TRANSFORMING GROWTH FACTOR BETA --METABOLISM -
E23	4	TRANSFORMING GROWTH FACTOR BETA --ORAL DRUG AD
E24	1	TRANSFORMING GROWTH FACTOR BETA --PARENTERAL D

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Ref	Items	Index-term
E25	75	TRANSFORMING GROWTH FACTOR BETA --PHARMACEUTIC
E26	3	TRANSFORMING GROWTH FACTOR BETA --PHARMACOECON
E27	62	TRANSFORMING GROWTH FACTOR BETA --PHARMACOKINE
E28	14529	TRANSFORMING GROWTH FACTOR BETA --PHARMACOLOGY
E29	6647	TRANSFORMING GROWTH FACTOR BETA --PHYSIOLOGY -
E30	63	TRANSFORMING GROWTH FACTOR BETA --RADIATION EF
E31	678	TRANSFORMING GROWTH FACTOR BETA --SECRETION --
E32	4	TRANSFORMING GROWTH FACTOR BETA --STANDARDS --
E33	4	TRANSFORMING GROWTH FACTOR BETA --SUBCUTANEOUS
E34	597	TRANSFORMING GROWTH FACTOR BETA --THERAPEUTIC
E35	13	TRANSFORMING GROWTH FACTOR BETA --TOPICAL DRUG
E36	102	TRANSFORMING GROWTH FACTOR BETA --TOXICITY --T

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Ref	Items	RT	Index-term
E37	131		TRANSFORMING GROWTH FACTOR BETA --URINE --UR
E38	4517		TRANSFORMING GROWTH FACTOR BETA //RECEPTORS,
E39	1		TRANSFORMING GROWTH FACTOR BETA ACTIVATED
E40	1		TRANSFORMING GROWTH FACTOR BETA ACTIVATED BIND
E41	62	6	TRANSFORMING GROWTH FACTOR BETA ACTIVATED KINA
E42	2		TRANSFORMING GROWTH FACTOR BETA ACTIVATED PROT
E43	1		TRANSFORMING GROWTH FACTOR BETA ACTIVATING KIN
E44	1		TRANSFORMING GROWTH FACTOR BETA ACTIVATION
E45	1		TRANSFORMING GROWTH FACTOR BETA ACTIVATOR PROT
E46	1		TRANSFORMING GROWTH FACTOR BETA ACTIVIN RECEPT
E47	1		TRANSFORMING GROWTH FACTOR BETA ACTIVIN RESPON
E48	1		TRANSFORMING GROWTH FACTOR BETA ACTIVITY

Enter P or PAGE for more

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Ref	Items	Index-term
E49	1	TRANSFORMING GROWTH FACTOR BETA ALPHA

E50 10 TRANSFORMING GROWTH FACTOR BETA ANTAGONIST
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Ref	Items	RT	Index-term
E1	10		TRANSFORMING GROWTH FACTOR BETA ANTAGONIST
E2	196	8	TRANSFORMING GROWTH FACTOR BETA ANTIBODY
E3	3		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --ADV
E4	6		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --CLI
E5	56		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --DRU
E6	4		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --END
E7	12		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --INT
E8	59		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --PHA
E9	3		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --SUB
E10	1		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --TOP
E11	1		TRANSFORMING GROWTH FACTOR BETA ASSOCIATED KIN
E12	1		TRANSFORMING GROWTH FACTOR BETA ASSOCIATED PEP

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Ref	Items	Index-term
E13	7	TRANSFORMING GROWTH FACTOR BETA BINDING PROTEI
E14	1	TRANSFORMING GROWTH FACTOR BETA CARTILAGE REGU
E15	1	TRANSFORMING GROWTH FACTOR BETA CDNA
E16	1	TRANSFORMING GROWTH FACTOR BETA COMPLEMENTARY
E17	2	TRANSFORMING GROWTH FACTOR BETA CONTROL ELEMEN
E18	2	TRANSFORMING GROWTH FACTOR BETA DERIVATIVE
E19	1	TRANSFORMING GROWTH FACTOR BETA EPIDERMAL GROW
E20	2	TRANSFORMING GROWTH FACTOR BETA FAMILY
E21	3	TRANSFORMING GROWTH FACTOR BETA FAMILY MEMBER
E22	2	TRANSFORMING GROWTH FACTOR BETA FAMILY MEMBERS
E23	1	TRANSFORMING GROWTH FACTOR BETA FAMILY OF SECR
E24	1	TRANSFORMING GROWTH FACTOR BETA FSH IMMUNOREAC

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Ref	Items	Index-term
E25	2	TRANSFORMING GROWTH FACTOR BETA GENE
E26	2	TRANSFORMING GROWTH FACTOR BETA GENES
E27	1	TRANSFORMING GROWTH FACTOR BETA GROWTH FACTOR
E28	1	TRANSFORMING GROWTH FACTOR BETA I RECEPTOR
E29	1	TRANSFORMING GROWTH FACTOR BETA I TGFBI
E30	11	TRANSFORMING GROWTH FACTOR BETA I 125
E31	2	TRANSFORMING GROWTH FACTOR BETA I-ASSOCIATED P
E32	1	TRANSFORMING GROWTH FACTOR BETA II
E33	5	TRANSFORMING GROWTH FACTOR BETA II RECEPTOR
E34	1	TRANSFORMING GROWTH FACTOR BETA II RECEPTOR IM
E35	2	TRANSFORMING GROWTH FACTOR BETA IMMUNOGLOBULIN
E36	1	TRANSFORMING GROWTH FACTOR BETA IMMUNOHISTOCHE

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Ref	Items	Index-term
E37	1	TRANSFORMING GROWTH FACTOR BETA IMMUNOSUPPRESS
E38	1	TRANSFORMING GROWTH FACTOR BETA INDUCED FACTOR
E39	3	TRANSFORMING GROWTH FACTOR BETA INDUCED GENE
E40	1	TRANSFORMING GROWTH FACTOR BETA INDUCED GENE H
E41	4	TRANSFORMING GROWTH FACTOR BETA INDUCIBLE EARL
E42	5	TRANSFORMING GROWTH FACTOR BETA INDUCIBLE GENE

E43	1	TRANSFORMING GROWTH FACTOR BETA INDUCIBLE IMME
E44	1	TRANSFORMING GROWTH FACTOR BETA INDUCIBLE PROT
E45	1	TRANSFORMING GROWTH FACTOR BETA INHIBITED MEMB
E46	4	TRANSFORMING GROWTH FACTOR BETA INHIBITOR
E47	1	TRANSFORMING GROWTH FACTOR BETA INHIBITORY ELE
E48	1	TRANSFORMING GROWTH FACTOR BETA ISOFORM

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Ref	Items	Index-term
E49	1	TRANSFORMING GROWTH FACTOR BETA ISOFORM OVEREX
E50	3	TRANSFORMING GROWTH FACTOR BETA ISOFORMS

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S1	3	'TRANSFORMING GROWTH FACTOR BETA ISOFORMS'
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Ref	Items	RT	Index-term
E1	3		TRANSFORMING GROWTH FACTOR BETA ISOFORMS
E2	1		TRANSFORMING GROWTH FACTOR BETA L
E3	1	1	TRANSFORMING GROWTH FACTOR BETA LATENCY ASSOCI
E4	1		TRANSFORMING GROWTH FACTOR BETA LATENCY BINDIN
E5	1		TRANSFORMING GROWTH FACTOR BETA LIKE BINDING P
E6	9		TRANSFORMING GROWTH FACTOR BETA MASKING PROTEI
E7	1		TRANSFORMING GROWTH FACTOR BETA MEMBER
E8	4		TRANSFORMING GROWTH FACTOR BETA MESSENGER RNA
E9	1		TRANSFORMING GROWTH FACTOR BETA MONOCLONAL ANT
E10	1		TRANSFORMING GROWTH FACTOR BETA MONONUCLEAR MA
E11	1		TRANSFORMING GROWTH FACTOR BETA MRNA TGF-BETA
E12	3		TRANSFORMING GROWTH FACTOR BETA MRNA TRANSFORM

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Ref	Items	Index-term
E13	3	TRANSFORMING GROWTH FACTOR BETA NEUTRALIZING A
E14	1	TRANSFORMING GROWTH FACTOR BETA ONE
E15	1	TRANSFORMING GROWTH FACTOR BETA ONE (TGF-BETA(
E16	1	TRANSFORMING GROWTH FACTOR BETA OSTEOCALCIN CO
E17	1	TRANSFORMING GROWTH FACTOR BETA PALATE MORPHOG
E18	1	TRANSFORMING GROWTH FACTOR BETA PATHWAY
E19	1	TRANSFORMING GROWTH FACTOR BETA PDGFR
E20	1	TRANSFORMING GROWTH FACTOR BETA PLATELET DERIV
E21	1	TRANSFORMING GROWTH FACTOR BETA PLATELET FACTO
E22	1	TRANSFORMING GROWTH FACTOR BETA PLATELET-DERIV
E23	1	TRANSFORMING GROWTH FACTOR BETA POLYPEPTIDE
E24	61	TRANSFORMING GROWTH FACTOR BETA PRECURSOR

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Ref	Items	RT	Index-term
E25	2		TRANSFORMING GROWTH FACTOR BETA PROTEIN
E26	1		TRANSFORMING GROWTH FACTOR BETA PSEUDORECEPTOR
E27	2287	7	TRANSFORMING GROWTH FACTOR BETA RECEPTOR
E28	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR --ADV
E29	2		TRANSFORMING GROWTH FACTOR BETA RECEPTOR --CLI
E30	53		TRANSFORMING GROWTH FACTOR BETA RECEPTOR --DRU
E31	1439		TRANSFORMING GROWTH FACTOR BETA RECEPTOR --END
E32	13		TRANSFORMING GROWTH FACTOR BETA RECEPTOR --INT
E33	45		TRANSFORMING GROWTH FACTOR BETA RECEPTOR --PHA

E34	1	TRANSFORMING GROWTH FACTOR BETA RECEPTOR --SUB
E35	2	TRANSFORMING GROWTH FACTOR BETA RECEPTOR --TOP
E36	1	TRANSFORMING GROWTH FACTOR BETA RECEPTOR AGONI

Enter P or PAGE for more

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Ref	Items	RT	Index-term
E37	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ALK1
E38	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ALK2
E39	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ALK5
E40	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ALK8
E41	7		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ANTAG
E42	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ASSOC
E43	2		TRANSFORMING GROWTH FACTOR BETA RECEPTOR BLOCK
E44	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR EXPRE
E45	6		TRANSFORMING GROWTH FACTOR BETA RECEPTOR FAMIL
E46	20		TRANSFORMING GROWTH FACTOR BETA RECEPTOR I
E47	3		TRANSFORMING GROWTH FACTOR BETA RECEPTOR I KIN
E48	34	1	TRANSFORMING GROWTH FACTOR BETA RECEPTOR II

Enter P or PAGE for more

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Ref	Items	Index-term
E49	1	TRANSFORMING GROWTH FACTOR BETA RECEPTOR II GE
E50	1	TRANSFORMING GROWTH FACTOR BETA RECEPTOR II TG

? p

Ref	Items	RT	Index-term
E1	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR II TG
E2	8		TRANSFORMING GROWTH FACTOR BETA RECEPTOR III
E3	2		TRANSFORMING GROWTH FACTOR BETA RECEPTOR INHIB
E4	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR INTER
E5	3		TRANSFORMING GROWTH FACTOR BETA RECEPTOR KINAS
E6	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR MESSE
E7	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR TGF-B
E8	25	1	TRANSFORMING GROWTH FACTOR BETA RECEPTOR TYPE
E9	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR V
E10	40		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 1
E11	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 1 KIN
E12	133	5	TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2

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Ref	Items	RT	Index-term
E13	2		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2 --D
E14	65		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2 --E
E15	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2 --I
E16	3		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2 --P
E17	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2 MES
E18	7		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 3
E19	2		TRANSFORMING GROWTH FACTOR BETA RECEPTOR (S)
E20	32	3	TRANSFORMING GROWTH FACTOR BETA RECEPTORS
E21	1		TRANSFORMING GROWTH FACTOR BETA REGULATORY ELE
E22	1		TRANSFORMING GROWTH FACTOR BETA RELATED PROTEI
E23	2		TRANSFORMING GROWTH FACTOR BETA RESPONSE ELEME
E24	1		TRANSFORMING GROWTH FACTOR BETA RESPONSIVE ELE

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Ref	Items	Index-term
E25	1	TRANSFORMING GROWTH FACTOR BETA RI
E26	1	TRANSFORMING GROWTH FACTOR BETA RII
E27	1	TRANSFORMING GROWTH FACTOR BETA RIL
E28	1	TRANSFORMING GROWTH FACTOR BETA SECRETION
E29	1	TRANSFORMING GROWTH FACTOR BETA SIGNAL MEDIATO
E30	2	TRANSFORMING GROWTH FACTOR BETA SIGNAL TRANSDU
E31	6	TRANSFORMING GROWTH FACTOR BETA SIGNALING
E32	5	TRANSFORMING GROWTH FACTOR BETA SIGNALING PATH
E33	1	TRANSFORMING GROWTH FACTOR BETA SIGNALLING PAT
E34	1	TRANSFORMING GROWTH FACTOR BETA SIMULATED CLON
E35	1	TRANSFORMING GROWTH FACTOR BETA SOLUBLE RECEPT
E36	4	TRANSFORMING GROWTH FACTOR BETA STIMULATED CLO

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?

? e transforming growth factor beta IV

Ref	Items	RT	Index-term
E1	1		TRANSFORMING GROWTH FACTOR BETA ISOFORM OVEREX
E2	3		TRANSFORMING GROWTH FACTOR BETA ISOFORMS
E3	0		*TRANSFORMING GROWTH FACTOR BETA IV
E4	1		TRANSFORMING GROWTH FACTOR BETA L
E5	1	1	TRANSFORMING GROWTH FACTOR BETA LATENCY ASSOCI
E6	1		TRANSFORMING GROWTH FACTOR BETA LATENCY BINDIN
E7	1		TRANSFORMING GROWTH FACTOR BETA LIKE BINDING P
E8	9		TRANSFORMING GROWTH FACTOR BETA MASKING PROTEI
E9	1		TRANSFORMING GROWTH FACTOR BETA MEMBER
E10	4		TRANSFORMING GROWTH FACTOR BETA MESSENGER RNA
E11	1		TRANSFORMING GROWTH FACTOR BETA MONOCLONAL ANT
E12	1		TRANSFORMING GROWTH FACTOR BETA MONONUCLEAR MA

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? e tgfb4

Ref	Items	Index-term
E1	1	TGFB3/MSX1 MARKERS
E2	1	TGFB3VARIANT
E3	21	*TGFB4
E4	1	TGFB47
E5	1	TGFB5
E6	8	TGFC
E7	1	TGFCARS
E8	1	TGFCDIA
E9	2	TGFCYS
E10	1	TGFCYSSUP33SER
E11	1	TGFCYS33
E12	2	TGFCYS33SER

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? s e3

S2 21 'TGFB4'

? e tgfb-4

Ref	Items	Index-term
E1	3	TGFB-3
E2	3	TGFB-3R

E3	0	*TGFB-4
E4	1	TGFB/G1
E5	5	TGFBA
E6	2	TGFBATA
E7	1	TGFBATTA1
E8	1	TGFBBA1
E9	1	TGFBETA
E10	1	TGFBETA1
E11	1	TGFBBR2
E12	4	TGFBE

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Ref	Items	Index-term
E13	3	TGFBEAT
E14	1	TGFBEATA1
E15	1	TGFBEAT1
E16	3	TGFBEP
E17	1	TGFBET
E18	14995	TGFBETA
E19	1	TGFBETA ACTIVATED KINASE TAK1 TRANSFORMING GRO
E20	1	TGFBETA BETA RECEPTOR TYPE II
E21	1	TGFBETA EXPRESSION
E22	2	TGFBETA FAMILY
E23	1	TGFBETA FAMILY SIGNALING
E24	1	TGFBETA GROWTH FACTOR

Enter P or PAGE for more

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Ref	Items	Index-term
E25	1	TGFBETA HP75 CELLS
E26	1	TGFBETA INDUCED CLONE H3
E27	1	TGFBETA INHIBITOR TUMOR GROWTH FACTOR BETA INH
E28	1	TGFBETA ISOFORMS
E29	1	TGFBETA MODULATION
E30	8	TGFBETA RECEPTOR
E31	1	TGFBETA RECEPTOR I
E32	1	TGFBETA RECEPTOR II
E33	12	TGFBETA RECEPTORS
E34	4	TGFBETA SIGNAL TRANSDUCTION
E35	11	TGFBETA SIGNALING
E36	1	TGFBETA SIGNALING PATHWAY

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Ref	Items	Index-term
E37	1	TGFBETA SIGNALING PATHWAYS
E38	6	TGFBETA SIGNALLING
E39	1	TGFBETA SIGNALS
E40	1	TGFBETA STEROID RECEPTORS
E41	6	TGFBETA SUPERFAMILY
E42	1	TGFBETA TRANSFORMING GROWTH FACTOR BETA
E43	1	TGFBETA TRANSFORMING GROWTH FACTOR BETA TRANSF
E44	2	TGFBETA TYPE I RECEPTOR
E45	3	TGFBETA TYPE II RECEPTOR
E46	1	TGFBETA TYPE II RECEPTOR PROMOTER
E47	1	TGFBETA TYPE II RECEPTOR SIGNALING
E48	1	TGFBETA VARIANTS

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Ref	Items	Index-term
E49	2	TGFBETA (TRANSFORMING GROWTH FACTOR BETA)
E50	1	TGFBETA)

? s e48

S3	1	'TGFBETA VARIANTS'
----	---	--------------------

? p

Ref	Items	Index-term
E1	1	TGFBETA)
E2	1	TGFBETA- 1
E3	2	TGFBETA-DEPENDENT
E4	1	TGFBETA-IIR
E5	1	TGFBETA-INDEPENDENT
E6	2	TGFBETA-INDUCED
E7	1	TGFBETA-INDUCIBLE GENE H3 (BETAIG-H3)
E8	1	TGFBETA-PATHWAY
E9	1	TGFBETA-RECEPTOR INTERACTING PROTEIN-1
E10	3	TGFBETA-RII
E11	1	TGFBETA-RII CELL LINE (HOMINIDAE)
E12	1	TGFBETA-SIGNALING

Enter P or PAGE for more

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Ref	Items	Index-term
E13	1	TGFBETA-SIGNALLING
E14	2	TGFBETA-SUPERFAMILY
E15	1	TGFBETA-TREATED
E16	7	TGFBETA-1
E17	1	TGFBETA-1 LASER MICRODISSECTION
E18	1	TGFBETA-1 TRANSFORMING GROWTH FACTOR BETA-1
E19	3	TGFBETA-2
E20	1	TGFBETA-3
E21	2	TGFBETA, TRANSFORMING GROWTH FACTOR BETA
E22	1	TGFBETA, TRANSFORMING GROWTH FACTOR-BETA
E23	2	TGFBETAA
E24	1	TGFBETAAND

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Ref	Items	Index-term
E25	3	TGFBETABETA1
E26	2	TGFBETAB2
E27	1	TGFBETACALCITROIL
E28	11	TGFBETAC10
E29	11	TGFBETAC25
E30	1	TGFBETAEPSILON
E31	1	TGFBETAFNSHOWED
E32	1	TGFBETAFNSKELETAL
E33	1	TGFBETAFNTREATMENT
E34	36	TGFBETAI
E35	1	TGFBETAIGH3
E36	20	TGFBETAI1

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Ref	Items	Index-term
E37	1	TGFBETAI II
E38	38	TGFBETAI IR
E39	1	TGFBETAIN
E40	430	TGFBETAINF
E41	12	TGFBETAINF 1
E42	1	TGFBETAINF 3
E43	1	TGFBETAINF 4
E44	7	TGFBETAI R
E45	1	TGFBETAI SOFORMS
E46	16	TGFBETAL
E47	1	TGFBETAMU
E48	1	TGFBETAOVER

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Ref	Items	Index-term
E49	3	TGFBETAP
E50	2	TGFBETAPRII

? p

Ref	Items	Index-term
E1	2	TGFBETAPRII
E2	113	TGFBETAR
E3	1	TGFBETAR II (A) 10
E4	1	TGFBETAR II (GT) 3
E5	7	TGFBETARE
E6	1	TGFBETARECEPTER
E7	2	TGFBETARECEPTOR
E8	1	TGFBETARECEPTORS
E9	1	TGFBETARES
E10	123	TGFBETARI
E11	610	TGFBETARII
E12	1	TGFBETARII FRAMESHIFT MUTATION

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Ref	Items	Index-term
E13	5	TGFBETARI IDELTAKD
E14	16	TGFBETARI III
E15	7	TGFBETARS
E16	1	TGFBETARSUB1
E17	20	TGFBETAR1
E18	4	TGFBETAR11
E19	30	TGFBETAR2
E20	10	TGFBETAR3
E21	446	TGFBETAS
E22	4	TGFBETASFR2
E23	1	TGFBETASIGNALING
E24	1	TGFBETASL

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Ref	Items	Index-term
E25	3	TGFBETASR
E26	7	TGFBETASRII
E27	183	TGFBETASUB1

E28	1	TGFBETASUB1STIMULATED
E29	40	TGFBETASUB2
E30	1	TGFBETASUB2TGFBETASUB2
E31	17	TGFBETASUB3
E32	3	TGFBETASUP
E33	1	TGFBETASUPERFAMILY
E34	1	TGFBETASUPPRESSED
E35	4	TGFBETASUP1
E36	4	TGFBETAS1

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Ref	Items	Index-term
E37	1	TGFBETATGFBETA
E38	1	TGFBETATO
E39	3	TGFBETATYPE
E40	7500	TGFBETA1
E41	1	TGFBETA1 - TRANSFORMING GROWTH FACTOR BETA
E42	1	TGFBETA1 DIFFERENTIATION
E43	1	TGFBETA1 GENE
E44	1	TGFBETA1 MRNA
E45	1	TGFBETA1 OVEREXPRESSION
E46	1	TGFBETA1 RECEPTORS
E47	1	TGFBETA1-ACTIVATED
E48	1	TGFBETA1ALPHAMP

Enter P or PAGE for more

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Ref	Items	Index-term
E49	1	TGFBETA1ANGIOTENSINII
E50	1	TGFBETA1AVAILABILITY

? p

Ref	Items	Index-term
E1	1	TGFBETA1AVAILABILITY
E2	1	TGFBETA1CDNA
E3	1	TGFBETA1DURING
E4	1	TGFBETA1GENE
E5	1	TGFBETA1KIDNEY
E6	1	TGFBETA1L
E7	2	TGFBETA1LAP
E8	4	TGFBETA1MRNA
E9	2	TGFBETA1POSITIVE
E10	1	TGFBETA1PRODUCING
E11	11	TGFBETA1R
E12	1	TGFBETA1REQUIRE

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Ref	Items	Index-term
E13	7	TGFBETA1RI
E14	7	TGFBETA1RII
E15	6	TGFBETA1SUP
E16	2	TGFBETA1SUPS223
E17	2	TGFBETA1SUPWT
E18	1	TGFBETA1SUP32
E19	1	TGFBETA1TRANSGENE
E20	1	TGFBETA1WERE

E21	1402	TGFBETA2
E22	1	TGFBETA2, IL-1
E23	1	TGFBETA2HUMAN
E24	5	TGFBETA2R

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Ref	Items	Index-term
E25	14	TGFBETA2SUP
E26	934	TGFBETA3
E27	1	TGFBETA3-ELISA
E28	1	TGFBETA3R
E29	1	TGFBETA3RII
E30	10	TGFBETA3SUP
E31	30	TGFBETA4
E32	14	TGFBETA5
E33	2	TGFBETE
E34	1	TGFBETGA1
E35	1	TGFBGR
E36	375	TGFBI

Enter P or PAGE for more

? s e31

S4	30	'TGFBETA4'
----	----	------------

? p

Ref	Items	Index-term
E37	1	TGFBI (BETA IG-H3) GENE
E38	1	TGFBI (BIGH3) GENE
E39	5	TGFBI BIGH3 GENE
E40	15	TGFBI GENE
E41	1	TGFBI TRANSFORMING GROWTH FACTOR-BETA-1
E42	1	TGFBI(BIGH3) GENE
E43	1	TGFBI-INDUCED
E44	2	TGFBIGENE
E45	9	TGFBII
E46	1	TGFBIII
E47	6	TGFBIIIR
E48	44	TGFBIIIR

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Ref	Items	Index-term
E49	1	TGFBIIIR GENE
E50	1	TGFBINDUCES

? p

Ref	Items	Index-term
E1	1	TGFBINDUCES
E2	7	TGFBINF
E3	2	TGFBIN3
E4	19	TGFBIP
E5	7	TGFBKM2
E6	2	TGFBKM2SUP129
E7	2	TGFBKM2129
E8	11	TGFBL
E9	7	TGFBM1
E10	6	TGFBM3
E11	25	TGFBP

E12 1 TGFBP-3

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Ref	Items	Index-term
E13	2	TGFBPS
E14	1	TGFBP1
E15	1	TGFBP3
E16	1	TGFBP4
E17	1	TGFBP5
E18	27	TGFBP
E19	1	TGFBP-SMAD
E20	1	TGFBP-SMAD SUPERFAMILY
E21	11	TGFBP1
E22	11	TGFBP1 PROTEIN, HUMAN
E23	21	TGFBP
E24	111	TGFBP

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? s el6

S5 1 'TGFBP4'

? p

Ref	Items	Index-term
E25	1	TGFBP GENE
E26	1	TGFBP GENE TRANSFORMING GROWTH FACTOR-BETA R
E27	3	TGFBP
E28	2	TGFBP
E29	1	TGFBP
E30	6	TGFBP
E31	6	TGFBP
E32	1	TGFBP
E33	2	TGFBP
E34	163	TGFBP
E35	1	TGFBP GENE
E36	1	TGFBP KINASE

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Ref	Items	Index-term
E37	1	TGFBP TRANSFORMING GROWTH FACTOR, BETA RECEPT
E38	4	TGFBP-ASTERISK-6A
E39	1	TGFBP-6A ALLELE
E40	2	TGFBP16A
E41	463	TGFBP2
E42	9	TGFBP2 GENE
E43	1	TGFBP2 GENE TYPE II TRANSFORMING GROWTH FACTOR
E44	13	TGFBP2 PROTEIN, HUMAN
E45	2	TGFBP2-RESTORED
E46	1	TGFBP2FLOXE2
E47	2	TGFBP2FLX
E48	4	TGFBP2FSPKO

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Ref	Items	Index-term
E49	1	TGFBP2HEPKO
E50	1	TGFBP2L

? e lefty 1

Ref	Items	Index-term
E1	1	LEFTY SIGNALING
E2	1	LEFTY VENTRICULAR REMODELING
E3	0	*LEFTY 1
E4	1	LEFTY 1 PROTEIN
E5	1	LEFTY- 1
E6	4	LEFTY-A
E7	1	LEFTY-A ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
E8	1	LEFTY-A MRNA
E9	1	LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
E10	2	LEFTY-B
E11	1	LEFTY-DEPENDENT
E12	1	LEFTY-GENE RELATED PRODUCT

Enter P or PAGE for more

? s e4-e10

	1	LEFTY 1 PROTEIN
	1	LEFTY- 1
	4	LEFTY-A
	1	LEFTY-A ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
	1	LEFTY-A MRNA
	1	LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
	2	LEFTY-B
S6	8	E4-E10

? p

Ref	Items	Index-term
E13	1	LEFTY-RELATED
E14	1	LEFTY-SIGNALING
E15	13	LEFTY-1
E16	5	LEFTY-1 GENE
E17	1	LEFTY-1 PROTEIN
E18	12	LEFTY-2
E19	3	LEFTY-2 GENE
E20	1	LEFTY-2 ISOLATION
E21	1	LEFTY-2 PROTEIN
E22	34	LEFTYA
E23	1	LEFTYA GENE
E24	1	LEFTYA PROTEIN

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? s e15 or e17 or e18 or e20 or e21 or e22 or e24

	13	LEFTY-1
	1	LEFTY-1 PROTEIN
	12	LEFTY-2
	1	LEFTY-2 ISOLATION
	1	LEFTY-2 PROTEIN
	34	LEFTYA
	1	LEFTYA PROTEIN
S7	57	'LEFTY-1' OR 'LEFTY-1 PROTEIN' OR 'LEFTY-2' OR 'LEFTY-2 ISOLATION' OR 'LEFTY-2 PROTEIN' OR 'LEFTYA' OR 'LEFTYA PROTEIN'

? p

Ref	Items	Index-term
E25	2	LEFTYB
E26	1	LEFTYB PROTEIN
E27	5	LEFTYL
E28	1	LEFTYRAY

E29	2	LEFTYS
E30	204	LEFTY1
E31	3	LEFTY1 GENE
E32	1	LEFTY1 PROTEIN
E33	1	LEFTY1GENE
E34	6	LEFTY1LEFTY2
E35	1	LEFTY1LEFTY2 TUBULIN MUTANT
E36	4	LEFTY1SUP

Enter P or PAGE for more

? s e25-e26 or e30 or e32 or e34 or e35 or e36

2	LEFTYB
1	LEFTYB PROTEIN
204	LEFTY1
1	LEFTY1 PROTEIN
6	LEFTY1LEFTY2
1	LEFTY1LEFTY2 TUBULIN MUTANT
4	LEFTY1SUP

S8 206 E25-E26 OR E30 OR E32 OR E34 OR E35 OR E36

? p

Ref	Items	Index-term
E37	196	LEFTY2
E38	3	LEFTY2 GENE
E39	1	LEFTY2 PROTEIN
E40	1	LEFTY2GENE
E41	1	LEFTY3
E42	1	LEFTY69
E43	4	LEFT1
E44	1	LEFU
E45	91	LEFUA
E46	1	LEFUA (OSTEICHTHYES)
E47	6	LEFUA COSTATA
E48	6	LEFUA COSTATA (OSTEICHTHYES)

Enter P or PAGE for more

? s e37 or e39

196	LEFTY2
1	LEFTY2 PROTEIN
S9 196	'LEFTY2' OR 'LEFTY2 PROTEIN'

? p

Ref	Items	Index-term
E49	1	LEFUA COSTATA ECHIGONIA
E50	1	LEFUA COSTATA MITOCHONDRIAL D-LOOP REGION GENE

? e lefty a

Ref	Items	Index-term
E1	929	LEFTY
E2	1	*LEFTY A
E3	6	LEFTY GENE
E4	1	LEFTY KREH'S ULTIMATE GUIDE TO FLY FISHING (BO
E5	2	LEFTY MUTANTS
E6	1	LEFTY POPULATION
E7	155	LEFTY PROTEIN
E8	1	LEFTY PROTEIN FAMILY
E9	4	LEFTY PROTEINS
E10	1	LEFTY SECRETED FACTORS
E11	1	LEFTY SEQUENCE
E12	1	LEFTY SIGNALING

Enter P or PAGE for more
? s e2 or e7 or e8 or e9

	1	LEFTY A
	155	LEFTY PROTEIN
	1	LEFTY PROTEIN FAMILY
	4	LEFTY PROTEINS
S10	161	'LEFTY A' OR 'LEFTY PROTEIN' OR 'LEFTY PROTEIN FAMILY' OR 'LEFTY PROTEINS'

? p

Ref	Items	Index-term
E13	1	LEFTY VENTRICULAR REMODELING
E14	1	LEFTY 1 PROTEIN
E15	1	LEFTY- 1
E16	4	LEFTY-A
E17	1	LEFTY-A ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
E18	1	LEFTY-A MRNA
E19	1	LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
E20	2	LEFTY-B
E21	1	LEFTY-DEPENDENT
E22	1	LEFTY-GENE RELATED PRODUCT
E23	1	LEFTY-RELATED
E24	1	LEFTY-SIGNALING

Enter P or PAGE for more
? s e14 or e15 or e16 or e17 or e18 or e19 or e20

	1	LEFTY 1 PROTEIN
	1	LEFTY- 1
	4	LEFTY-A
	1	LEFTY-A ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
	1	LEFTY-A MRNA
	1	LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
	2	LEFTY-B
S11	8	'LEFTY 1 PROTEIN' OR 'LEFTY- 1' OR 'LEFTY-A' OR 'LEFTY-A ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR' OR 'LEFTY-A MRNA' OR 'LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR' OR 'LEFTY-B'

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Set	Items	Description
S1	3	'TRANSFORMING GROWTH FACTOR BETA ISOFORMS'
S2	21	'TGFB4'
S3	1	'TGFBETA VARIANTS'
S4	30	'TGFBETA4'
S5	1	'TGFBP4'
S6	8	E4-E10
S7	57	'LEFTY-1' OR 'LEFTY-1 PROTEIN' OR 'LEFTY-2' OR 'LEFTY-2 IS- OLATION' OR 'LEFTY-2 PROTEIN' OR 'LEFTYA' OR 'LEFTYA PROTEIN'
S8	206	E25-E26 OR E30 OR E32 OR E34 OR E35 OR E36
S9	196	'LEFTY2' OR 'LEFTY2 PROTEIN'
S10	161	'LEFTY A' OR 'LEFTY PROTEIN' OR 'LEFTY PROTEIN FAMILY' OR - 'LEFTY PROTEINS'
S11	8	'LEFTY 1 PROTEIN' OR 'LEFTY- 1' OR 'LEFTY-A' OR 'LEFTY-A E- NDOMETRIAL BLEEDING-ASSOCIATED FACTOR' OR 'LEFTY-A MRNA' OR '- LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR' OR 'LEFTY-B'

?

? s s1 or s2 or s3 or s4 or s5 or s6 or s7 or s8 or s9 or s10 or s11

3	S1
21	S2
1	S3
30	S4

1 S5
8 S6
57 S7
206 S8
196 S9
161 S10
8 S11
S12 531 S1 OR S2 OR S3 OR S4 OR S5 OR S6 OR S7 OR S8 OR S9 OR S10
OR S11

? s s12/1996:2005

Processing

Processed 10 of 26 files ...

>>>One or more prefixes are unsupported

>>> or undefined in one or more files.

>>>Year ranges not supported in one or more files

Processing

Completed processing all files

531 S12
49727561 PY=1996 : PY=2005
S13 525 S12/1996:2005

? s s12 not s13

531 S12
525 S13
S14 6 S12 NOT S13

?

? rd

...completed examining records

S15 4 RD (unique items)

? t s15/6/all

15/6/1 (Item 1 from file: 71)
00304408 95125590

The immunomodulatory diversity of the proteins of the transforming growth
factor beta (TGFbetaP) family
PUBLICATION DATE: 19950000

15/6/2 (Item 2 from file: 71)
00290512 95107663

Expression of transforming growth factor beta in the embryonic avian lens
coincides with the presence of mitochondria
PUBLICATION DATE: 19950000

15/6/3 (Item 1 from file: 144)
10488633 PASCAL No.: 92-0692127
Localization of the human insulin-like growth-factor-binding protein 4
gene to chromosomal region 17q12-21.1
1992

15/6/4 (Item 1 from file: 399)
DIALOG(R)File 399:(c) 2005 American Chemical Society. All rts. reserv.

Complementary deoxyribonucleic acid cloning of a messenger ribonucleic
acid encoding transforming growth factor .beta. 4 from chicken embryo
chondrocytes

? t s15/9/1 2 3

15/9/1 (Item 1 from file: 71)

DIALOG(R)File 71:ELSEVIER BIOBASE
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00304408 95125590

The immunomodulatory diversity of the proteins of the transforming growth factor beta (TGFbetaP) family

Wieczorek Z.; Sion J.; Kluczyk A.; Zbozien R.; Stafanowicz P.; Siemion I.Z.
ADDRESS: Z. Wieczorek, L. Hirschfeld Inst Immun/Exp Therapy, Polish Academy
of Sciences, Czerska 12, 53-114 Wroclaw, Poland

Journal: International Journal of Peptide and Protein Research, 46/2
(113-118), 1995, Denmark

PUBLICATION DATE: 19950000

CODEN: IJPPC

ISSN: 0367-8377

DOCUMENT TYPE: Article

LANGUAGES: English SUMMARY LANGUAGES: English

The examination of immunomodulatory properties of oligopeptides derived from two exposed loops (containing thymopentin-like and tuftsin-like sequences, respectively) of the proteins belonging to TGFbeta family suggests that the particular species of the TGFbeta family should differ distinctly in their influence on the immune response. According to our results obtained from three TGFbeta species of mammals, TGFbeta 2 should be a strong immunosuppressor, whereas for TGFbeta 3 the immunostimulative potency is more probable. TGFbeta 1 species would possess both immunosuppressive and immunostimulative potency, residing in two different loops of the protein. The results obtained also suggest that chicken TGFbeta4 should be associated with immunostimulative effects and xenopus TGFbeta5 with immunosuppressive ones.

DESCRIPTORS:

Peptide immunomodulators; Thymopentin-like sequences; Transforming growth factor beta; Tuftsin-like sequences

CLASSIFICATION CODE AND DESCRIPTION:

89.2.4.5 - CELL AND DEVELOPMENTAL BIOLOGY / CELL GROWTH AND DIVISION /
Growth Factors and Inhibitors / Transforming growth factors (TGF)

86.5.4.6 - IMMUNOLOGY AND INFECTIOUS DISEASES / HUMORAL MEDIATORS OF IMMUNE
RESPONSE / Other Factors / Haematopoietic growth factors (CSF)

15/9/2 (Item 2 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE
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00290512 95107663

Expression of transforming growth factor beta in the embryonic avian lens coincides with the presence of mitochondria

Potts J.D.; Bassnett S.; Beebe D.C.

ADDRESS: J.D. Potts, Department of Anatomy/Cell Biology, Uniformed Svcs.
Univ. of Health Sci., 4301 Jones Bridge Road, Bethesda, MD
20814-4799, United States

Journal: Developmental Dynamics, 203/3 (317-323), 1995, United States

PUBLICATION DATE: 19950000

CODEN: DEDYE

ISSN: 1058-8388

DOCUMENT TYPE: Article

LANGUAGES: English SUMMARY LANGUAGES: English

During their maturation, lens cells lose all membrane bound organelles, including mitochondria. In chicken embryos this process begins in the

central lens fibers beginning around embryonic day 12 (E12). Transforming growth factor beta (TGFbeta) is a multipotent growth modulator thought to play a role in numerous developmental processes. TGFbeta1 has been localized to mitochondria in rat liver cells and muscle cells. In the present study, we examined the expression of TGFbeta isoform mRNAs and proteins during chicken embryonic lens development. PCR analysis demonstrated TGFbeta2 and TGFbeta3 transcripts in the lens epithelium and fibers throughout pre- and post-hatching development. TGFbeta isoforms were detected throughout the lens epithelium and fibers early in development (E6). However by E19, the distribution of TGFbeta2 and TGFbeta3 transcripts and proteins coincided with regions of the lens that contained mitochondria. In addition, intense TGFbeta staining was observed in the basal portions of the equatorial epithelial cells, a region with abundant mitochondria. Transcripts for TGFbeta1 and TGFbeta4 were not detected in any tissue or time frame examined. Similarly, no immunostaining for TGFbeta1 was observed.

DESCRIPTORS:

TGFbeta; Chicken lens; Lens differentiation; Mitochondria

CLASSIFICATION CODE AND DESCRIPTION:

89.8.9.7 - CELL AND DEVELOPMENTAL BIOLOGY / DEVELOPMENT (BY TISSUE AND ORGAN SYSTEMS) / Nervous System / Sensory - visual
89.2.4.5 - CELL AND DEVELOPMENTAL BIOLOGY / CELL GROWTH AND DIVISION / Growth Factors and Inhibitors / Transforming growth factors (TGF)
89.1.8.7 - CELL AND DEVELOPMENTAL BIOLOGY / MEMBRANES AND CELL TRANSPORT / Cytoplasmic Membranes / Mitochondria

15/9/3 (Item 1 from file: 144)

DIALOG(R) File 144:Pascal

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10488633 PASCAL No.: 92-0692127

Localization of the human insulin-like growth-factor-binding protein 4 gene to chromosomal region 17q12-21.1

BAJALICA S; ALLANDER S V; EHRENBORG E; BRONDUM-NIELSEN K; LUTTMAN H; LARSSON C

Karolinska hosp., dep. clinical genetics, 10401 Stockholm, Sweden

Journal: Human genetics, 1992, 89 (2) 234-236

ISSN: 0340-6717 CODEN: HUGEDQ Availability: INIST-2672;

354000028118920170

No. of Refs.: 13 ref.

Document Type: P (Serial) ; A (Analytic)

Country of Publication: Federal Republic of Germany

Language: English

Insulin-like growth-factor-binding proteins (IGFBPs) constitute a family of structurally related proteins that specifically bind insulin-like growth factors and modulate their functions. In this study, the chromosomal localization was determined for the gene encoding IGFBP4, i.e. inhibitory-IGFBP. A polymerase chain reaction (PCR) fragment corresponding to the previously published cDNA sequence was used to isolate overlapping cosmid clones. By fluorescent in situ hybridization to metaphase chromosomes, the IGFBP4 gene was then localized to chromosomal region 17q21-21.1

English Descriptors: E17-Chromosome; Binding protein; Genetic mapping;

Human; Somatomedin C; Insulin like growth factor 2; Polymerase chain

reaction; Molecular hybridization; In situ; Molecular biology; Genetics;

Exploration

French Descriptors: Chromosome E17; Proteine liaison; Carte genetique;
Homme; Somatomedine C; Facteur croissance IGF2; Reaction chaine
polymerase; Hybridation moleculaire; In situ; Biologie moleculaire;
Genetique; Exploration

Classification Codes: 002A07C03

? t s15/9/4

15/9/4 (Item 1 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

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111091468 CA: 111(11)91468h JOURNAL

Complementary deoxyribonucleic acid cloning of a messenger ribonucleic
acid encoding transforming growth factor .beta. 4 from chicken embryo
chondrocytes

AUTHOR(S): Jakowlew, Sonia B.; Dillard, Pamela J.; Sporn, Michael B.;
Roberts, Anita B.

LOCATION: Lab. Chemoprev., Natl. Cancer Inst., Bethesda, MD, 20892, USA

JOURNAL: Mol. Endocrinol. DATE: 1988 VOLUME: 2 NUMBER: 12 PAGES:
1186-95 CODEN: MOENEN ISSN: 0888-8809 LANGUAGE: English

SECTION:

CA203003 Biochemical Genetics

CA202XXX Mammalian Hormones

CA213XXX Mammalian Biochemistry

IDENTIFIERS: cDNA cloning sequencing chicken TGFbeta4, transforming
growth factor chicken gene sequence

DESCRIPTORS:

Gene and Genetic element, animal...

for transforming growth factor .beta.4, of chicken, nucleotide and
encoded peptide sequences of

Animal growth regulators, .beta.4-transforming growth factors...

gene for, of chicken, nucleotide and encoded peptide sequences of
Deoxyribonucleic acid sequences, .beta.4-transforming growth
factor-specifying...

of chicken, multiple clones, complete

Protein sequences...

of transforming growth factor .beta.4 and precursor, multiple clones,
complete

Molecular cloning...

of transforming growth factor .beta.4 cDNA, of chicken

Chicken...

transforming growth factor .beta.4 gene of, nucleotide and encoded
peptide sequences of

CAS REGISTRY NUMBERS:

122319-69-1 122319-70-4 amino acid sequence of

122318-73-4 nucleotide sequence of

? logoff hold

26sep05 07:24:19 User228206 Session D2511.2

\$2.83 0.832 DialUnits File155

\$2.83 Estimated cost File155

\$5.35 0.907 DialUnits File5

\$5.35 Estimated cost File5

\$29.30 1.323 DialUnits File34

\$29.30 Estimated cost File34

\$0.87 0.211 DialUnits File35

\$0.87 Estimated cost File35

\$1.06 0.198 DialUnits File48

\$1.06 Estimated cost File48

\$5.17 1.378 DialUnits File65

\$5.17 Estimated cost File65
 \$5.25 0.600 DialUnits File71
 \$0.00 2 Type(s) in Format 6
 \$4.00 2 Type(s) in Format 9
 \$4.00 4 Types
 \$9.25 Estimated cost File71
 \$7.54 0.709 DialUnits File73
 \$7.54 Estimated cost File73
 \$0.38 0.089 DialUnits File91
 \$0.38 Estimated cost File91
 \$1.93 0.553 DialUnits File94
 \$1.93 Estimated cost File94
 \$0.87 0.205 DialUnits File98
 \$0.87 Estimated cost File98
 \$0.81 0.150 DialUnits File135
 \$0.81 Estimated cost File135
 \$3.68 0.819 DialUnits File144
 \$0.00 1 Type(s) in Format 6
 \$1.65 1 Type(s) in Format 9
 \$1.65 2 Types
 \$5.33 Estimated cost File144
 \$1.14 0.259 DialUnits File149
 \$1.14 Estimated cost File149
 \$1.77 0.300 DialUnits File156
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 \$0.95 0.300 DialUnits File159
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 \$0.89 Estimated cost File162
 \$0.45 0.130 DialUnits File164
 \$0.45 Estimated cost File164
 \$1.45 0.136 DialUnits File172
 \$1.45 Estimated cost File172
 \$0.29 0.082 DialUnits File266
 \$0.29 Estimated cost File266
 \$0.43 0.123 DialUnits File369
 \$0.43 Estimated cost File369
 \$0.36 0.102 DialUnits File370
 \$0.36 Estimated cost File370
 \$13.95 1.112 DialUnits File399
 \$0.55 1 Type(s) in Format 6
 \$2.75 1 Type(s) in Format 9
 \$3.30 2 Types
 \$17.25 Estimated cost File399
 \$2.57 0.116 DialUnits File434
 \$2.57 Estimated cost File434
 \$0.33 0.068 DialUnits File444
 \$0.33 Estimated cost File444
 \$0.61 0.096 DialUnits File467
 \$0.61 Estimated cost File467
 OneSearch, 26 files, 10.996 DialUnits FileOS
 \$2.66 TELNET
 \$101.84 Estimated cost this search
 \$101.84 Estimated total session cost 11.207 DialUnits

Logoff: level 0
 You are now logged off

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Search for

*probe
encode
0099-713*

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 15 AA

Date run: 2005-09-24 15:42:21 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,312,053 sequences; 758,486,757 total letters

UniProt Knowledgebase Release 6.0 consists of:

UniProtKB/Swiss-Prot Release 48.0 of 13-Sep-2005: 194317 entries

UniProtKB/TrEMBL Release 31.0 of 13-Sep-2005: 2105517 entries

[Taxonomic view](#)

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[Printable view](#)

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db AC	Description	Score	E-value
<input type="checkbox"/> sp P50414	TGFB1_SHEEP Transforming growth factor beta 1 precurs...	53	6e-07
<input type="checkbox"/> sp P17246	TGFB1_RAT Transforming growth factor beta 1 precursor ...	53	6e-07
<input type="checkbox"/> sp P07200	TGFB1_PIG Transforming growth factor beta 1 precursor ...	53	6e-07
<input type="checkbox"/> sp P04202	TGFB1_MOUSE Transforming growth factor beta 1 precurs...	53	6e-07
<input type="checkbox"/> sp P01137	TGFB1_HUMAN Transforming growth factor beta 1 precurs...	53	6e-07
<input type="checkbox"/> sp O19011	TGFB1_HORSE Transforming growth factor beta 1 precurs...	53	6e-07
<input type="checkbox"/> sp P09533	TGFB1_CERAE Transforming growth factor beta 1 precurs...	53	6e-07
<input type="checkbox"/> sp P54831	TGFB1_CANFA Transforming growth factor beta 1 precurs...	53	6e-07
<input type="checkbox"/> sp P18341	TGFB1_BOVIN Transforming growth factor beta 1 precurs...	53	6e-07

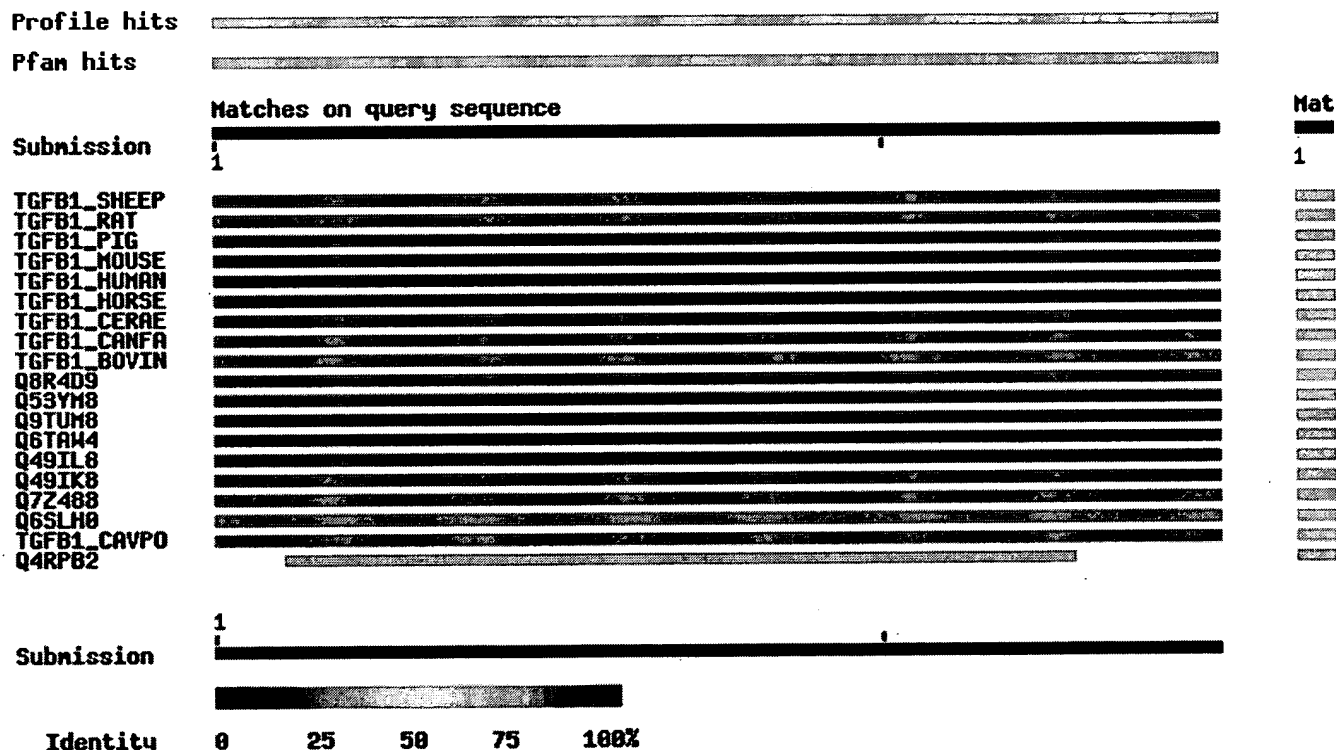
<input type="checkbox"/>	tr Q8R4D9	_SIGHI Transforming growth factor beta-1 protein (Fragm...	53	6e-07
<input type="checkbox"/>	tr Q53YM8	_RAT TGF beta 1 [Rattus norvegicus (Rat)]	53	6e-07
<input type="checkbox"/>	tr Q9TUM8	_HORSE Transforming growth factor beta 1 [TGFB1] [Equus...	53	6e-07
<input type="checkbox"/>	tr Q6TAW4	_FELCA TGF beta (Fragment) [Felis silvestris catus (Cat)]	53	6e-07
<input type="checkbox"/>	tr Q49IL8	_HUMAN Transforming growth factor beta 1 precursor (Fra...	53	6e-07
<input type="checkbox"/>	tr Q49IK8	_HUMAN Transforming growth factor beta 1 precursor (Fra...	53	6e-07
<input type="checkbox"/>	tr Q7Z488	_HUMAN Transforming growth factor beta 1 precursor (Fra...	53	6e-07
<input type="checkbox"/>	tr Q6SLH0	_PERMA Transforming growth factor beta 1 (Fragment) [Tg...	50	5e-06
<input type="checkbox"/>	sp Q9Z1Y6	TGFB1_CAVPO Transforming growth factor beta 1 precurs...	50	7e-06
<input type="checkbox"/>	tr Q4RPB2	_TETNG Chromosome 1 SCAF15008, whole genome shotgun seq...	32	2.1

Graphical overview of the alignments

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Alignments

sp P50414 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_SHEEP [TGFB1] AA
 [Ovis aries (Sheep)] align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp P17246 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_RAT [Tgfb1] AA
[Rattus norvegicus (Rat)] [align](#)

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp P07200 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_PIG [TGFB1] AA
[Sus scrofa (Pig)] [align](#)

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp P04202 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_MOUSE [Tgfb1] AA
[Mus musculus (Mouse)] [align](#)

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp P01137 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_HUMAN [TGFB1] AA
[Homo sapiens (Human)] [align](#)

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp O19011 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_HORSE [TGFB1] AA
[Equus caballus (Horse)] [align](#)

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp P09533 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_CERAE [TGFB1] AA
[Cercopithecus aethiops (Green monkey) (Grivet)] [align](#)

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp P54831 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_CANFA [TGFB1] AA
[Canis familiaris (Dog)] [align](#)

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp P18341 Transforming growth factor beta 1 precursor (TGF-beta 1) 315 AA
TGFB1_BOVIN (Fragment) [TGFB1] [Bos taurus (Bovine)]
[align](#)

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 24 PEADYYAKEVTRVLM 38

tr Q8R4D9 Transforming growth factor beta-1 protein (Fragment) 368
Q8R4D9_SIGHI [Tgfb1] AA
[Sigmodon hispidus (Hispid cotton rat)] align

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 77 PEADYYAKEVTRVLM 91

tr Q53YM8 TGF beta 1 [Rattus norvegicus (Rat)] 390 AA
Q53YM8_RAT align

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

tr Q9TUM8 Transforming growth factor beta 1 [TGFB1] [Equus 390
Q9TUM8_HORSE caballus (Horse)] AA
align

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

tr Q6TAW4 TGF beta (Fragment) [Felis silvestris catus (Cat)] 226 AA
Q6TAW4_FELCA align

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 50 PEADYYAKEVTRVLM 64

tr Q49IL8 Transforming growth factor beta 1 precursor (Fragment) 118
Q49IL8_HUMAN [TGFB1] AA
[Homo sapiens (Human)] align

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

tr Q49IK8 Transforming growth factor beta 1 precursor (Fragment) 118
Q49IK8_HUMAN [TGFB1] AA
[Homo sapiens (Human)] [align](#)

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

tr Q7Z488 Transforming growth factor beta 1 precursor (Fragment) 118
Q7Z488_HUMAN [TGFB1] AA
[Homo sapiens (Human)] [align](#)

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

tr Q6SLH0 Transforming growth factor beta 1 (Fragment) [Tgfb1] 249
Q6SLH0_PERMA [Peromyscus
maniculatus (Deer mouse)] AA
[align](#)

Score = 50.3 bits (111), Expect = 5e-06
Identities = 14/15 (93%), Positives = 14/15 (93%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 65 PETDYYAKEVTRVLM 79

sp Q9Z1Y6 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_CAVPO [TGFB1] AA
[Cavia porcellus (Guinea pig)] [align](#)

Score = 49.8 bits (110), Expect = 7e-06
Identities = 14/15 (93%), Positives = 14/15 (93%)

Query: 1 PEADYYAKEVTRVLM 15
PE DYYAKEVTRVLM
Sbjct: 99 PEPDYYAKEVTRVLM 113

tr Q4RPB2 Chromosome 1 SCAF15008, whole genome shotgun sequence. 454
Q4RPB2_TETNG (Fragment) AA
[GSTENG00031190001] [Tetraodon nigroviridis (Green align
puffer)]

Score = 31.6 bits (67), Expect = 2.1
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 2 EADYYAKEVTRV 13
E DYYAKEV R+
Sbjct: 96 EEDYYAKEVQRI 107

Database: EXPASY/UniProtKB
Posted date: Sep 12, 2005 12:34 PM
Number of letters in database: 758,486,757
Number of sequences in database: 2,312,053

Lambda	K	H
0.329	0.280	1.74

Gapped		
Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of HSP's successfully gapped in prelim test: 0
length of query: 15
length of database: 758,486,757
effective HSP length: 6
effective length of query: 9
effective length of database: 744,614,439
effective search space: 6701529951
effective search space used: 6701529951
T: 16
A: 40
X1: 15 (7.1 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 42 (21.8 bits)
S2: 62 (29.5 bits)

Wallclock time: 2 seconds

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ESVEPEPEP

sp|P50414|TGFB1_SHEEP
sp|O19011|TGFB1_HORSE
sp|P18341|TGFB1_BOVIN
sp|P09531|TGFB1_CHICK

GQILSKLRLASPPSQGDVPPGPLPEAILALYNSTRDRVAG-ESAETEPEP
GQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRAQVAG-ESAETEPEP
-----AILALYNSTRDRVAG-ESAETEPEP
GQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLKQARLRPPPDG

: *****: : : *

sp|P07200|TGFB1_PIG

EADYYAKEVTRVLMLESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVL

 [ExPASy Home page](#) [Site Map](#) [Search ExPASy](#) [Contact us](#) [Proteomics tools](#) [Swiss-Prot](#)

Search for

SIB BLAST Network Service

This NCBI BLAST2 service is maintained by the [Swiss Institute of Bioinformatics](#).

Click on the  icons to access the [online BLAST help](#).

Accession number or sequence

Enter a Swiss-Prot/TrEMBL accession number or a **PROTEIN** sequence in **RAW** format.

QHVELYQKYS NNS


HTML

Output format:

or

Choose the appropriate BLAST  program and  database:

 **blastp** - query against the UniProt Knowledgebase (Swiss-Prot + TrEMBL)

 Taxonomic groups (not available for PDB and translated EST):

select a

database

subsection

or specify

a

taxonomic
group

To restrict the search to a particular taxon, it is much faster to select drop-down list on the left than to specify your own taxonomic group; more accurate statistics.

Enter a species name, a TaxID or the latin name of a taxonomic group (OX lines) to restrict your search to a particular taxon. You may enter (";"). Example: Fungi; Homo sapiens.

or select a
microbial
proteome

Ab to epitope
Bovine
aa 91-107

☐ Search only Swiss-Prot (curated sequences) ☐ Exclude fragment sequences

☐ **blastp** - query against another protein database Please, supply an email address if y

☐ **tblastn** - query against the six-frame translation of a nucleotide database

Taxonomic groups:

or select a

microbial

genome

☐ Your email address:

If an e-mail address is provided, results will be automatically mailed back (recommended for tblastn searches).

or

Options:

☐ Comparison Matrix:

Number of best scoring sequences to show:

Number of best alignments to show:

☐ Setting the E threshold: (Number of expected matches in a random database)

☐ ☒ Filter the sequence for low-complexity regions

☐ ☒ Gapped alignment

☐ ☐ Identity BLAST

For a more 'advanced' BLAST2 search (with more options and programs, and a larger variety of databases) please use the [original submission form at EMBnet-CH \(Lausanne\)](#).

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If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query: 13 AA

Date run: 2005-09-24 15:53:30 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,312,053 sequences; 758,486,757 total letters

UniProt Knowledgebase Release 6.0 consists of:

UniProtKB/Swiss-Prot Release 48.0 of 13-Sep-2005: 194317 entries

UniProtKB/TrEMBL Release 31.0 of 13-Sep-2005: 2105517 entries

[Taxonomic view](#)

[NiceBlast view](#)

[Printable view](#)

List of potentially matching sequences

Send selected sequences to

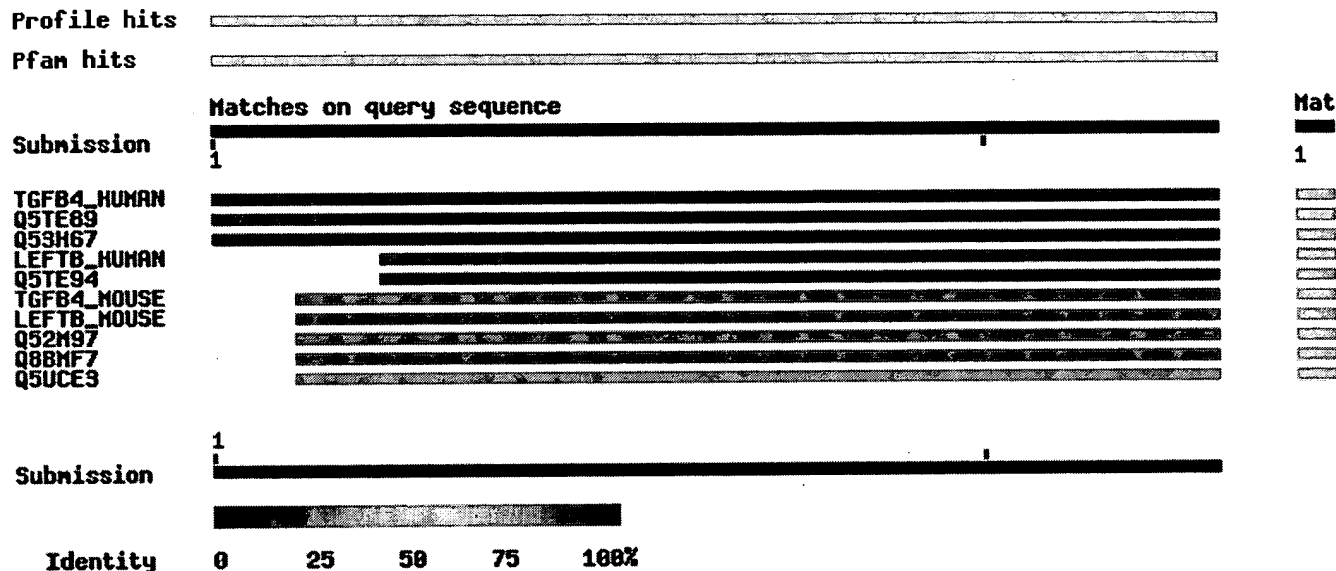
☐ Include query sequence

	Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp	O00292	TGFB4_HUMAN Transforming growth factor beta 4 precurs...	43	6e-04
<input type="checkbox"/>	tr	Q5TE89	_HUMAN Left-right determination factor 2 [LEFTY2] [Homo...	43	6e-04
<input type="checkbox"/>	tr	Q53H67	_HUMAN Left-right determination, factor B preproprotein...	43	6e-04
<input type="checkbox"/>	sp	O75610	LEFTB_HUMAN Left-right determination factor B precurs...	38	0.019
<input type="checkbox"/>	tr	Q5TE94	_HUMAN Left-right determination factor 1 [LEFTY1] [Homo...	38	0.019
<input type="checkbox"/>	sp	Q64280	TGFB4_MOUSE Transforming growth factor beta 4 precurs...	38	0.025
<input type="checkbox"/>	sp	P57785	LEFTB_MOUSE Left-right determination factor B precurs...	38	0.025
<input type="checkbox"/>	tr	Q52M97	_XENLA Hypothetical protein [Xenopus laevis (African cl...	38	0.025
<input type="checkbox"/>	tr	Q8BMF7	_MOUSE Mus musculus 13 days embryo male testis cDNA, RI...	38	0.025

☐ tr Q5UCE3 _RAT EBAF precursor [Rattus norvegicus (Rat)]

35 0.20

Graphical overview of the alignments

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Alignments

sp O00292 Transforming growth factor beta 4 precursor (TGF-beta 4) 366 AA
 TGFB4_HUMAN (Endometrial bleeding-associated factor) (Left-right
 determination factor A) (Lefty-A protein) [EBAF] [Homo sapiens (Human)] [align](#)

Score = 43.5 bits (95), Expect = 6e-04
 Identities = 13/13 (100%), Positives = 13/13 (100%)

Query: 1 ASEASTHLLVFGM 13
 ASEASTHLLVFGM
 Sbjct: 91 ASEASTHLLVFGM 103

tr Q5TE89 Left-right determination factor 2 [LEFTY2] [Homo sapiens] 366
 Q5TE89_HUMAN (Human)] AA
[align](#)

Score = 43.5 bits (95), Expect = 6e-04
 Identities = 13/13 (100%), Positives = 13/13 (100%)

Query: 1 ASEASTHLLVFGM 13
 ASEASTHLLVFGM
 Sbjct: 91 ASEASTHLLVFGM 103

tr Q53H67 Left-right determination, factor B preproprotein variant 366
Q53H67_HUMAN (Fragment) AA
[LEFTY1] [Homo sapiens (Human)] [align](#)

Score = 43.5 bits (95), Expect = 6e-04
Identities = 13/13 (100%), Positives = 13/13 (100%)

Query: 1 ASEASTHLLVFGM 13
ASEASTHLLVFGM
Sbjct: 91 ASEASTHLLVFGM 103

sp O75610 Left-right determination factor B precursor (Lefty-B 366
LEFTB_HUMAN protein) AA
[LEFTB] [Homo sapiens (Human)] [align](#)

Score = 38.4 bits (83), Expect = 0.019
Identities = 11/11 (100%), Positives = 11/11 (100%)

Query: 3 EASTHLLVFGM 13
EASTHLLVFGM
Sbjct: 93 EASTHLLVFGM 103

tr Q5TE94 Left-right determination factor 1 [LEFTY1] [Homo sapiens 366
Q5TE94_HUMAN (Human)] AA
[align](#)

Score = 38.4 bits (83), Expect = 0.019
Identities = 11/11 (100%), Positives = 11/11 (100%)

Query: 3 EASTHLLVFGM 13
EASTHLLVFGM
Sbjct: 93 EASTHLLVFGM 103

sp Q64280 Transforming growth factor beta 4 precursor (TGF-beta 4) 368
TGFB4_MOUSE (Lefty AA
protein) (Lefty-1 protein) (STRA3 protein) [Ebaf] [Mus [align](#)
musculus (Mouse)]

Score = 38.0 bits (82), Expect = 0.025
Identities = 11/12 (91%), Positives = 11/12 (91%)

Query: 2 SEASTHLLVFGM 13
SE STHLLVFGM
Sbjct: 92 SETSTHLLVFGM 103

sp P57785 Left-right determination factor B precursor (Lefty-2 368
LEFTB_MOUSE protein) AA
[Leftb] [Mus musculus (Mouse)] [align](#)

Score = 38.0 bits (82), Expect = 0.025
Identities = 11/12 (91%), Positives = 11/12 (91%)

Query: 2 SEASTHLLVFGM 13
SE STHLLVFGM
Sbjct: 92 SETSTHLLVFGM 103

tr Q52M97 Hypothetical protein [Xenopus laevis (African clawed 368
Q52M97_XENLA frog)] AA
[align](#)

Score = 38.0 bits (82), Expect = 0.025
Identities = 11/12 (91%), Positives = 11/12 (91%)

Query: 2 SEASTHLLVFGM 13
SE STHLLVFGM
Sbjct: 92 SETSTHLLVFGM 103

tr Q8BMF7 Mus musculus 13 days embryo male testis cDNA, RIKEN 368
Q8BMF7_MOUSE full-length AA
enriched library, clone:6030463A22 product:LEFT-RIGHT
DETERMINATION FACTOR B (LEFTY-2 PROTEIN), full insert
sequence (Left-right determination factor 2) [Lefty2]
[Mus musculus (Mouse)] [align](#)

Score = 38.0 bits (82), Expect = 0.025
Identities = 11/12 (91%), Positives = 11/12 (91%)

Query: 2 SEASTHLLVFGM 13
SE STHLLVFGM
Sbjct: 92 SETSTHLLVFGM 103

tr Q5UCE3 EBAF precursor [Rattus norvegicus (Rat)] 366 AA
Q5UCE3_RAT
[align](#)

Score = 35.0 bits (75), Expect = 0.20
Identities = 10/12 (83%), Positives = 10/12 (83%)

Query: 2 SEASTHLLVFGM 13
SE S HLLVFGM
Sbjct: 92 SETSSHLLVFGM 103

Database: EXPASY/UniProtKB
Posted date: Sep 12, 2005 12:34 PM

Number of letters in database: 758,486,757
Number of sequences in database: 2,312,053

Lambda	K	H
0.342	0.277	1.67

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of HSP's successfully gapped in prelim test: 0

length of query: 13

length of database: 758,486,757

effective HSP length: 4

effective length of query: 9

effective length of database: 749,238,545

effective search space: 6743146905

effective search space used: 6743146905

T: 16

A: 40

X1: 15 (7.4 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 40 (21.6 bits)

S2: 62 (29.5 bits)

Wallclock time: 2 seconds

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If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query: 13 AA

Date run: 2005-09-24 15:46:19 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,312,053 sequences; 758,486,757 total letters

UniProt Knowledgebase Release 6.0 consists of:

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UniProtKB/TrEMBL Release 31.0 of 13-Sep-2005: 2105517 entries

[Taxonomic view](#)

[NiceBlast view](#)

[Printable view](#)

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp	P07200 TGFB1_PIG Transforming growth factor beta 1 precursor ...	46	9e-05
<input type="checkbox"/>	sp	P01137 TGFB1_HUMAN Transforming growth factor beta 1 precurs...	42	0.001
<input type="checkbox"/>	sp	P09533 TGFB1_CERAE Transforming growth factor beta 1 precurs...	42	0.001
<input type="checkbox"/>	sp	P54831 TGFB1_CANFA Transforming growth factor beta 1 precurs...	42	0.001
<input type="checkbox"/>	tr	Q6TAW4 _FELCA TGF beta (Fragment) [Felis silvestris catus (Cat)]	42	0.001
<input type="checkbox"/>	tr	Q49IL8 _HUMAN Transforming growth factor beta 1 precursor (Fra...	42	0.001
<input type="checkbox"/>	tr	Q49IK8 _HUMAN Transforming growth factor beta 1 precursor (Fra...	42	0.001
<input type="checkbox"/>	tr	Q7Z488 _HUMAN Transforming growth factor beta 1 precursor (Fra...	42	0.001
<input type="checkbox"/>	sp	P17246 TGFB1_RAT Transforming growth factor beta 1 precursor ...	40	0.008

<input type="checkbox"/>	sp	P04202	TGFB1_MOUSE Transforming growth factor beta 1 precurs...	40	0.008
<input type="checkbox"/>	tr	Q8R4D9	_SIGHI Transforming growth factor beta-1 protein (Fragm...	40	0.008
<input type="checkbox"/>	tr	Q53YM8	_RAT TGF beta 1 [Rattus norvegicus (Rat)]	40	0.008
<input type="checkbox"/>	sp	Q9Z1Y6	TGFB1_CAVPO Transforming growth factor beta 1 precurs...	39	0.014
<input type="checkbox"/>	sp	P50414	TGFB1_SHEEP Transforming growth factor beta 1 precurs...	37	0.045
<input type="checkbox"/>	sp	O19011	TGFB1_HORSE Transforming growth factor beta 1 precurs...	37	0.045
<input type="checkbox"/>	sp	P18341	TGFB1_BOVIN Transforming growth factor beta 1 precurs...	37	0.045
<input type="checkbox"/>	tr	Q9TUM8	_HORSE Transforming growth factor beta 1 [TGFB1] [Equus...	37	0.045
<input type="checkbox"/>	tr	Q6SLH0	_PERMA Transforming growth factor beta 1 (Fragment) [Tg...	37	0.061
<input type="checkbox"/>	tr	Q68FX4	_RAT Hematopoietic cell specific Lyn substrate 1 (Predi...	34	0.48
<input type="checkbox"/>	tr	Q6T890	_ACTPL TonB2 [tonB2] [Actinobacillus pleuropneumoniae (...]	33	0.64
<input type="checkbox"/>	tr	Q4R7C6	_MACFA Testis cDNA, clone: QtsA-15617, similar to human...	33	0.64
<input type="checkbox"/>	sp	P14317	HCLS1_HUMAN Hematopoietic lineage cell specific protei...	33	0.86
<input type="checkbox"/>	tr	Q6IBK9	_HUMAN HCLS1 protein [HCLS1] [Homo sapiens (Human)]	33	0.86
<input type="checkbox"/>	tr	Q53Y93	_HUMAN Hematopoietic cell-specific Lyn substrate 1 [Hom...	33	0.86
<input type="checkbox"/>	tr	Q87MK6	_VIBPA Hypothetical protein VP2226 [VP2226] [Vibrio par...	32	1.1
<input type="checkbox"/>	tr	Q9EN57	_NPVST Zinc finger protein [Spodoptera litura multicaps...	32	1.5
<input type="checkbox"/>	tr	Q91BL1	_NPVST HOAR [Spodoptera litura multicapsid nucleopolyhe...	32	1.5
<input type="checkbox"/>	tr	Q8BGM6	_MOUSE Mus musculus 10 days neonate cerebellum cDNA, RI...	32	1.5
<input type="checkbox"/>	tr	Q80Z30	_RAT Calmodulin-dependent protein kinase phosphatase N ...	32	1.5
<input type="checkbox"/>	tr	Q5SX30	_MOUSE Protein phosphatase 1E (PP2C domain containing) ...	32	1.5
<input type="checkbox"/>	tr	Q80VJ8	_MOUSE Hypothetical protein BC050196 [BC050196] [Mus mu...	32	2.1
<input type="checkbox"/>	tr	Q6CE67	_YARLI Similarity [YALI0B18172g] [Yarrowia lipolytica (...]	32	2.1
<input type="checkbox"/>	tr	Q9VT49	_DROME CG14168-PA [CG14168] [Drosophila melanogaster (F...	31	2.8
<input type="checkbox"/>	tr	P91156	_CAEEL Hypothetical protein [C43E11.1] [Caenorhabditis ...]	31	2.8
<input type="checkbox"/>	tr	Q5KGJ5	_CRYNE Hypothetical protein [CNE03390] [Cryptococcus ne...	31	2.8
<input type="checkbox"/>	tr	Q55S44	_CRYNE Hypothetical protein [CNBE3380] [Cryptococcus ne...	31	2.8
<input type="checkbox"/>	tr	Q8I4T3	_PLAF7 PFG377 protein [PFL2405c] [Plasmodium falciparum...	31	3.7
<input type="checkbox"/>	tr	Q26022	_PLAFA Plasmodium falciparum sexual stage mRNA sequence...	31	3.7
<input type="checkbox"/>	tr	Q25857	_PLAFA Pfg377 [Plasmodium falciparum]	31	3.7
<input type="checkbox"/>	tr	Q7S935	_NEUCR Predicted protein [NCU07949.1] [Neurospora crassa]	31	3.7
<input type="checkbox"/>	tr	Q52FL1	_MAGGR Hypothetical protein [MG01625.4] [Magnaporthe gr...	31	3.7
<input type="checkbox"/>	sp	Q9D1X0	NOL3_MOUSE Nucleolar protein 3 [Nol3] [Mus musculus (M...	30	5.0
<input type="checkbox"/>	sp	Q8XRH0	FTSK1_RALSO DNA translocase ftsK 1 [ftsK1] [Ralstonia ...]	30	5.0
<input type="checkbox"/>	sp	Q9GLM6	APOE_HYLLA Apolipoprotein E precursor (Apo-E) [APOE] [...]	30	5.0
<input type="checkbox"/>	tr	Q8R2S3	_MOUSE Nucleolar protein 3 [Nol3] [Mus musculus (Mouse)]	30	5.0
<input type="checkbox"/>	tr	Q8C550	_MOUSE Mus musculus adult male hypothalamus cDNA, RIKEN...	30	5.0
<input type="checkbox"/>	tr	Q53YU5	_MOUSE Apoptosis repressor interacting with CARD (0 day...	30	5.0
<input type="checkbox"/>	tr	Q73XH7	_MYCPA Fas [fas] [Mycobacterium paratuberculosis]	30	5.0
<input type="checkbox"/>	tr	Q478V8	_9RHO0 Response regulator receiver:CheW-like protein:AT...	30	5.0
<input type="checkbox"/>	tr	Q9EXU1	_KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	5.0
<input type="checkbox"/>	tr	Q6XXM0	_MYCSM Fatty acid synthetase I [fas1] [Mycobacterium sm...	30	5.0
<input type="checkbox"/>	tr	Q5MBX2	_ACTSU TonB2 [tonB2] [Actinobacillus suis]	30	5.0
<input type="checkbox"/>	tr	Q4QZC1	_KLEPN Periplasmic energy transducer (Fragment) [tonB] ...	30	5.0
<input type="checkbox"/>	tr	Q9VAI5	_DROME CG15506-PB, isoform B [CG15506] [Drosophila mela...	30	5.0

<input type="checkbox"/>	tr	Q9N411	_CAEEL Prion-like-(Q/n-rich)-domain-bearing protein pro...	30	5.0
<input type="checkbox"/>	tr	Q8MZB6	_DROME AT15667p [CG15506] [Drosophila melanogaster (Fru...	30	5.0
<input type="checkbox"/>	tr	Q8IMK6	_DROME CG15506-PA, isoform A [CG15506] [Drosophila mela...	30	5.0
<input type="checkbox"/>	tr	Q4U8R9	_THEAN Hypothetical protein [TA10045] [Theileria annulata]	30	5.0
<input type="checkbox"/>	tr	Q5AQG7	_EMENI Hypothetical protein [AN9463.2] [Aspergillus nid...	30	5.0
<input type="checkbox"/>	tr	Q5ARP0	_EMENI Predicted protein [AN9040.2] [Aspergillus nidula...	30	5.0
<input type="checkbox"/>	tr	Q5ATE5	_EMENI Hypothetical protein [AN8435.2] [Aspergillus nid...	30	5.0
<input type="checkbox"/>	tr	Q527B1	_MAGGR Hypothetical protein [MG06645.4] [Magnaporthe gr...	30	5.0
<input type="checkbox"/>	tr	Q526E4	_MAGGR Hypothetical protein [MG06862.4] [Magnaporthe gr...	30	5.0
<input type="checkbox"/>	tr	Q4PFF2	_USTMA Hypothetical protein [UM01161.1] [Ustilago maydi...	30	5.0
<input type="checkbox"/>	tr	Q4IFF5	_GIBZE Hypothetical protein [FG04053.1] [Gibberella zea...	30	5.0
<input type="checkbox"/>	sp	P26185	TONB_SERMA TonB protein [tonB] [Serratia marcescens]	30	6.7
<input type="checkbox"/>	sp	P25945	TONB_SALTY TonB protein [tonB] [Salmonella typhimurium]	30	6.7
<input type="checkbox"/>	sp	P45610	TONB_KLEPN TonB protein [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	sp	P46383	TONB_ENTAE TonB protein [tonB] [Enterobacter aerogenes...	30	6.7
<input type="checkbox"/>	sp	P02929	TONB_ECOLI TonB protein [tonB] [Escherichia coli]	30	6.7
<input type="checkbox"/>	sp	Q62881	NOL3_RAT Nucleolar protein 3 [Nol3] [Rattus norvegicus...	30	6.7
<input type="checkbox"/>	sp	P97855	G3BP_MOUSE Ras-GTPase-activating protein binding prote...	30	6.7
<input type="checkbox"/>	tr	Q4SUQ6	_TETNG Chromosome undetermined SCAF13844, whole genome ...	30	6.7
<input type="checkbox"/>	tr	Q62882	_RAT Hypothetical protein [Rattus norvegicus (Rat)]	30	6.7
<input type="checkbox"/>	tr	Q5NCU1	_MOUSE Ras-GTPase-activating protein SH3-domain binding...	30	6.7
<input type="checkbox"/>	tr	Q571F9	_MOUSE MKIAA4115 protein (Fragment) [G3bp] [Mus musculu...	30	6.7
<input type="checkbox"/>	tr	Q57P65	_SALCH SsrAB activated gene [srfA] [Salmonella cholerae...	30	6.7
<input type="checkbox"/>	tr	Q57NS2	_SALCH Energy transducer; uptake of iron, cyanocobalimi...	30	6.7
<input type="checkbox"/>	tr	Q9S3M6	_BORPE TonB protein (Siderophore-mediated iron transpor...	30	6.7
<input type="checkbox"/>	tr	Q8Z7E4	_SALTI TonB protein [tonB] [Salmonella typhi]	30	6.7
<input type="checkbox"/>	tr	Q8XCC2	_ECO57 Energy transducer; uptake of iron, cyanocobalimi...	30	6.7
<input type="checkbox"/>	tr	Q8FHW5	_ECOL6 TonB protein [tonB] [Escherichia coli O6]	30	6.7
<input type="checkbox"/>	tr	Q885B3	_PSESM Major facilitator family transporter [PSPT01922]...	30	6.7
<input type="checkbox"/>	tr	Q884X6	_PSESM Flagellar assembly protein FliH, putative [PSPTO...	30	6.7
<input type="checkbox"/>	tr	Q83RM7	_SHIFL Membrane protein, energy transducer [tonB] [Shig...	30	6.7
<input type="checkbox"/>	tr	Q7WKX3	_BORBR Siderophore-mediated iron transport protein [ton...	30	6.7
<input type="checkbox"/>	tr	Q7W7I4	_BORPA Siderophore-mediated iron transport protein [ton...	30	6.7
<input type="checkbox"/>	tr	Q5PHV4	_SALPA Putative virulence effector protein [srfA] [Salm...	30	6.7
<input type="checkbox"/>	tr	Q5PCS7	_SALPA TonB protein [tonB] [Salmonella paratyphi-a]	30	6.7
<input type="checkbox"/>	tr	Q5NZS1	_AZOSE Translation initiation factor IF-2 [infB] [Azoar...	30	6.7
<input type="checkbox"/>	tr	Q48GE4	_PSESH Flagellar assembly protein FliH [fliH] [Pseudomo...	30	6.7
<input type="checkbox"/>	tr	Q9ZG18	_BORBR TonB [tonB] [Bordetella bronchiseptica (Alcalige...	30	6.7
<input type="checkbox"/>	tr	Q9S3Z9	_KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9S3Z7	_KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9S3Z6	_KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9R440	_KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9R427	_KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9R426	_KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9EXU0	_KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7

☐ tr Q9EXT9_KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae] 30 6.7

Graphical overview of the alignments

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([Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits

Pfam hits

Submission	Matches on query sequence	Mat
1	1	1
TGFB1_PIG		
TGFB1_HUMAN		
TGFB1_CERAE		
TGFB1_CANFA		
Q6TAN4		
Q49IL8		
Q49IK8		
Q7Z488		
TGFB1_RAT		
TGFB1_MOUSE		
Q8R4D9		
Q53YM8		
TGFB1_CAVPO		
TGFB1_SHEEP		
TGFB1_HORSE		
TGFB1_BOVIN		
Q9TUM8		
Q6SLH8		
Q68FX4		
Q6T890		
Q4R7C6		
HCLS1_HUMAN		
Q6IBK9		
Q53Y93		
Q87MK6		
Q9EN57		
Q91BL1		
Q8BGM6		
Q80Z30		
Q55X30		
Q88VJ8		
Q6CE67		
Q9VT49		
P91156		
Q5KGJ5		
Q55S44		
Q8I4T9		
Q26022		
Q25857		
Q75935		
Q52FL1		
NOL3_MOUSE		
FTSK1_RALSO		
APDE_HYLLA		
Q8R2S3		
Q8C558		
Q53YU5		
Q73XH7		
Q478V8		
Q9EXU1		
Q6XOM0		
Q5HBX2		
Q4QZC1		
Q9VAI5		
Q9N411		
Q8HZB6		
Q8INK6		
Q4U8R9		
Q5AQ67		
Q5ARP0		
Q5ATE5		
Q527B1		
Q526E4		
Q4PFF2		
Q4IFF5		
TONB_SERMA		
TONB_SALTY		
TONB_KLEPN		
TONB_ENTRE		
TONB_ECOLI		
NOL3_RAT		
G3BP_MOUSE		
Q4SU06		
Q62882		
Q5NCU1		
Q571F9		
Q57P65		
Q57NS2		
Q953H6		
Q8Z7E4		
Q8XCC2		
Q8FHM5		
Q885B3		
Q884X6		
Q83RM7		
Q7MKX9		

Alignments

sp P07200 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_PIG [TGFB1] AA
[Sus scrofa (Pig)] [align](#)

Score = 46.0 bits (101), Expect = 9e-05
Identities = 13/13 (100%), Positives = 13/13 (100%)

Query: 1 ESVEPEPEPEADY 13
ESVEPEPEPEADY
Sbjct: 91 ESVEPEPEPEADY 103

sp P01137 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_HUMAN [TGFB1] AA
[Homo sapiens (Human)] [align](#)

Score = 42.2 bits (92), Expect = 0.001
Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEADY 13
ES EPEPEPEADY
Sbjct: 91 ESAEPEPEPEADY 103

sp P09533 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_CERAE [TGFB1] AA
[Cercopithecus aethiops (Green monkey) (Grivet)] [align](#)

Score = 42.2 bits (92), Expect = 0.001
Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEADY 13
ES EPEPEPEADY
Sbjct: 91 ESAEPEPEPEADY 103

sp P54831 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_CANFA [TGFB1] AA
[Canis familiaris (Dog)] [align](#)

Score = 42.2 bits (92), Expect = 0.001
Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEADY 13
ES EPEPEPEADY
Sbjct: 91 ESAEPEPEPEADY 103

tr Q6TAW4 TGF beta (Fragment) [Felis silvestris catus (Cat)] 226 AA
Q6TAW4_FELCA

align

Score = 42.2 bits (92), Expect = 0.001
Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEADY 13
ES EPEPEPEADY
Sbjct: 42 ESAEPEPEPEADY 54

tr Q49IL8 Transforming growth factor beta 1 precursor (Fragment) 118
Q49IL8_HUMAN [TGFB1] AA
[Homo sapiens (Human)] align

Score = 42.2 bits (92), Expect = 0.001
Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEADY 13
ES EPEPEPEADY
Sbjct: 91 ESAEPEPEPEADY 103

tr Q49IK8 Transforming growth factor beta 1 precursor (Fragment) 118
Q49IK8_HUMAN [TGFB1] AA
[Homo sapiens (Human)] align

Score = 42.2 bits (92), Expect = 0.001
Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEADY 13
ES EPEPEPEADY
Sbjct: 91 ESAEPEPEPEADY 103

tr Q7Z488 Transforming growth factor beta 1 precursor (Fragment) 118
Q7Z488_HUMAN [TGFB1] AA
[Homo sapiens (Human)] align

Score = 42.2 bits (92), Expect = 0.001
Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEADY 13
ES EPEPEPEADY
Sbjct: 91 ESAEPEPEPEADY 103

sp P17246 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_RAT [Tgfb1] AA
[Rattus norvegicus (Rat)] align

Score = 39.7 bits (86), Expect = 0.008
Identities = 11/13 (84%), Positives = 12/13 (91%)

Query: 1 ESVEPEPEPEADY 13
ES +PEPEPEADY
Sbjct: 91 ESADPEPEPEADY 103

sp P04202 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_MOUSE [Tgfb1] AA
[Mus musculus (Mouse)] [align](#)

Score = 39.7 bits (86), Expect = 0.008
Identities = 11/13 (84%), Positives = 12/13 (91%)

Query: 1 ESVEPEPEPEADY 13
ES +PEPEPEADY
Sbjct: 91 ESADPEPEPEADY 103

tr Q8R4D9 Transforming growth factor beta-1 protein (Fragment) 368
Q8R4D9_SIGHI [Tgfb1] AA
[Sigmodon hispidus (Hispid cotton rat)] [align](#)

Score = 39.7 bits (86), Expect = 0.008
Identities = 11/13 (84%), Positives = 12/13 (91%)

Query: 1 ESVEPEPEPEADY 13
ES +PEPEPEADY
Sbjct: 69 ESADPEPEPEADY 81

tr Q53YM8 TGF beta 1 [Rattus norvegicus (Rat)] 390 AA
Q53YM8_RAT
[align](#)

Score = 39.7 bits (86), Expect = 0.008
Identities = 11/13 (84%), Positives = 12/13 (91%)

Query: 1 ESVEPEPEPEADY 13
ES +PEPEPEADY
Sbjct: 91 ESADPEPEPEADY 103

sp Q9Z1Y6 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_CAVPO [TGFB1] AA
[Cavia porcellus (Guinea pig)] [align](#)

Score = 38.8 bits (84), Expect = 0.014
Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 1 ESVEPEPEPEADY 13
ES EPEPEPE DY
Sbjct: 91 ESAEPEPEPEPDY 103

sp P50414 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_SHEEP [TGFB1] AA
[Ovis aries (Sheep)] [align](#)

Score = 37.1 bits (80), Expect = 0.045
Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 1 ESVEPEPEPEADY 13
ES E EPEPEADY
Sbjct: 91 ESAETEPEPEADY 103

sp O19011 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_HORSE [TGFB1] AA
[Equus caballus (Horse)] [align](#)

Score = 37.1 bits (80), Expect = 0.045
Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 1 ESVEPEPEPEADY 13
ES E EPEPEADY
Sbjct: 91 ESAETEPEPEADY 103

sp P18341 Transforming growth factor beta 1 precursor (TGF-beta 1) 315 AA
TGFB1_BOVIN (Fragment) [TGFB1] [Bos taurus (Bovine)]
[align](#)

Score = 37.1 bits (80), Expect = 0.045
Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 1 ESVEPEPEPEADY 13
ES E EPEPEADY
Sbjct: 16 ESAETEPEPEADY 28

tr Q9TUM8 Transforming growth factor beta 1 [TGFB1] [Equus 390
Q9TUM8_HORSE caballus (Horse)] AA
[align](#)

Score = 37.1 bits (80), Expect = 0.045
Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 1 ESVEPEPEPEADY 13
ES E EPEPEADY
Sbjct: 91 ESAETEPEPEADY 103

tr Q6SLH0 Transforming growth factor beta 1 (Fragment) [Tgfb1] 249
Q6SLH0_PERMA [Peromyscus
maniculatus (Deer mouse)] AA
[align](#)

Score = 36.7 bits (79), Expect = 0.061
Identities = 10/13 (76%), Positives = 11/13 (83%)

Query: 1 ESVEPEPEPEADY 13
ES +PEPEPE DY
Sbjct: 57 ESADPEPEPETDY 69

tr Q68FX4 Hematopoietic cell specific Lyn substrate 1 (Predicted) 476 AA
Q68FX4_RAT [Hcls1_predicted] [Rattus norvegicus (Rat)]
[align](#)

Score = 33.7 bits (72), Expect = 0.48
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
EPEPEPE DY
Sbjct: 369 EPEPEPEPDY 378

tr Q6T890 TonB2 [tonB2] [Actinobacillus pleuropneumoniae] 285
Q6T890_ACTPL (Haemophilus
pleuropneumoniae)] AA
[align](#)

Score = 33.3 bits (71), Expect = 0.64
Identities = 9/10 (90%), Positives = 10/10 (100%)

Query: 3 VEPEPEPEAD 12
VEPEPEPEA+
Sbjct: 73 VEPEPEPEAE 82

tr Q4R7C6 Testis cDNA, clone: QtsA-15617, similar to human 475
Q4R7C6_MACFA hematopoietic
cell-specific Lyn substrate 1 (HCLS1), mRNA, RefSeq: AA
NM_005335.3 [Macaca fascicularis (Crab eating macaque)]
(Cynomolgus monkey)] [align](#)

Score = 33.3 bits (71), Expect = 0.64
Identities = 11/16 (68%), Positives = 11/16 (68%), Gaps = 3/16 (18%)

Query: 1 ESV---EPEPEPEADY 13
E V EPEPEPE DY
Sbjct: 357 EPVYEAPEPEPENDY 372

sp P14317 Hematopoietic lineage cell specific protein 486
HCLS1_HUMAN (Hematopoietic AA
cell-specific LYN substrate 1) (LckBP1) (p75) [HCLS1] align
[Homo sapiens (Human)]

Score = 32.9 bits (70), Expect = 0.86
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
EPEPEPE DY
Sbjct: 369 EPEPEPENDY 378

tr Q6IBK9 HCLS1 protein [HCLS1] [Homo sapiens (Human)] 486 AA
Q6IBK9_HUMAN align

Score = 32.9 bits (70), Expect = 0.86
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
EPEPEPE DY
Sbjct: 369 EPEPEPENDY 378

tr Q53Y93 Hematopoietic cell-specific Lyn substrate 1 [Homo 486
Q53Y93_HUMAN sapiens (Human)] AA
align

Score = 32.9 bits (70), Expect = 0.86
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
EPEPEPE DY
Sbjct: 369 EPEPEPENDY 378

tr Q87MK6 Hypothetical protein VP2226 [VP2226] [Vibrio 370
Q87MK6_VIBPA parahaemolyticus] AA
align

Score = 32.5 bits (69), Expect = 1.1
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 2 SVEPEPEPE 10
.SVEPEPEPE
Sbjct: 43 SVEPEPEPE 51

tr Q9EN57 Zinc finger protein [Spodoptera litura multicapsid 497 AA

Q9EN57_NPVST nucleopolyhedrovirus (SpltMNPV)]

align

Score = 32.0 bits (68), Expect = 1.5
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 ESVEPEPEPE 10
ES EPEPEPE
Sbjct: 355 ESAEPEPEPE 364

tr Q91BL1 HOAR [Spodoptera litura multicapsid nucleopolyhedrovirus 731 AA
Q91BL1_NPVST. (SpltMNPV)]

align

Score = 32.0 bits (68), Expect = 1.5
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 ESVEPEPEPE 10
ES EPEPEPE
Sbjct: 459 ESAEPEPEPE 468

tr Q8BGM6 Mus musculus 10 days neonate cerebellum cDNA, RIKEN 151
Q8BGM6_MOUSE full-length AA
enriched library, clone:B930008A12 product:similar to align
PP2CH (Mus musculus 0 day neonate eyeball cDNA, RIKEN
full-length enriched library, clone:E130208E03
product:similar to PP2CH) [Ppm1e] [Mus musculus
(Mouse)]

Score = 32.0 bits (68), Expect = 1.5
Identities = 10/12 (83%), Positives = 11/12 (91%), Gaps = 1/12 (8%)

Query: 1 ESVEPEPEPEAD 12
ES EPEPEPEA+
Sbjct: 36 ES-EPEPEPEAE 46

tr Q80Z30 Calmodulin-dependent protein kinase phosphatase N [Ppm1e] 750
Q80Z30_RAT [Rattus AA
norvegicus (Rat)] align

Score = 32.0 bits (68), Expect = 1.5
Identities = 10/12 (83%), Positives = 11/12 (91%), Gaps = 1/12 (8%)

Query: 1 ESVEPEPEPEAD 12
ES EPEPEPEA+
Sbjct: 36 ES-EPEPEPEAE 46

tr Q5SX30 Protein phosphatase 1E (PP2C domain containing) [Ppm1e] 749
Q5SX30_MOUSE [Mus musculus (Mouse)] AA
align

Score = 32.0 bits (68), Expect = 1.5
Identities = 10/12 (83%), Positives = 11/12 (91%), Gaps = 1/12 (8%)

Query: 1 ESVEPEPEPEAD 12
ES EPEPEPEA+
Sbjct: 36 ES-EPEPEPEAE 46

tr Q80VJ8 Hypothetical protein BC050196 [BC050196] [Mus musculus] 578
Q80VJ8_MOUSE (Mouse)] AA
align

Score = 31.6 bits (67), Expect = 2.1
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 ESVEPEPEPE 10
E VEPEPEPE
Sbjct: 402 EEVEPEPEPE 411

tr Q6CE67 Similarity [YALI0B18172g] [Yarrowia lipolytica (Candida 1080 AA
Q6CE67_YARLI lipolytica)]
align

Score = 31.6 bits (67), Expect = 2.1
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 ESVEPEPEPE 10
E VEPEPEPE
Sbjct: 116 EEVEPEPEPE 125

tr Q9VT49 CG14168-PA [CG14168] [Drosophila melanogaster (Fruit 734
Q9VT49_DROME fly)] AA
align

Score = 31.2 bits (66), Expect = 2.8
Identities = 10/12 (83%), Positives = 10/12 (83%)

Query: 1 ESVEPEPEPEAD 12
E VEPEPEPE D
Sbjct: 348 EVVEPEPEPEKD 359

tr P91156 Hypothetical protein [C43E11.1] [Caenorhabditis elegans] 580 AA
P91156_CABEL
align

Score = 31.2 bits (66), Expect = 2.8
Identities = 10/12 (83%), Positives = 10/12 (83%), Gaps = 2/12 (16%)

Query: 3 VEPE--PEPEAD 12
 VEPE PEPEAD
Sbjct: 118 VEPEAEPEPEAD 129

tr Q5KGJ5 Hypothetical protein [CNE03390] [Cryptococcus neoformans 498 AA
 Q5KGJ5_CRYNE (Filobasidiella neoformans)]
[align](#)

Score = 31.2 bits (66), Expect = 2.8
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
 EPEPEPE +Y
Sbjct: 300 EPEPEPEPEY 309

tr Q55S44 Hypothetical protein [CNBE3380] [Cryptococcus neoformans 303
 Q55S44_CRYNE var.
 neoformans B-3501A]
[align](#)

Score = 31.2 bits (66), Expect = 2.8
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
 EPEPEPE +Y
Sbjct: 111 EPEPEPEPEY 120

tr Q8I4T3 PFG377 protein [PFL2405c] [Plasmodium falciparum 3119
 Q8I4T3_PLAF7 (isolate 3D7)]
[align](#)

Score = 30.8 bits (65), Expect = 3.7
Identities = 10/13 (76%), Positives = 11/13 (83%), Gaps = 1/13 (7%)

Query: 1 ESV-EPEPEPEAD 12
 E V EPEPEPEA+
Sbjct: 123 EEVREPEPEPEAE 135

tr Q26022 Plasmodium falciparum sexual stage mRNA sequence. 754
 Q26022_PLAFA (Fragment)
 [Plasmodium falciparum]
[align](#)

Score = 30.8 bits (65), Expect = 3.7
Identities = 10/13 (76%), Positives = 11/13 (83%), Gaps = 1/13 (7%)

sp Q8XRHO DNA translocase ftsK 1 [ftsK1] [Ralstonia solanacearum] 959
FTSK1_RALSO (Pseudomonas
solanacearum)] AA
align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 334 EPEPEPEAE 342

sp Q9GLM6 Apolipoprotein E precursor (Apo-E) [APOE] [Hylobates lar] 317
APOE_HYLLA (Common
gibbon)] AA
align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 1 ESVEPEPEPE 10
+ VEPEPEPE
Sbjct: 22 QAVEPEPEPE 31

tr Q8R2S3 Nucleolar protein 3 [Nol3] [Mus musculus (Mouse)] 220 AA
Q8R2S3_MOUSE
align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
EPEPEPE D+
Sbjct: 202 EPEPEPEPDF 211

tr Q8C550 Mus musculus adult male hypothalamus cDNA, RIKEN full- 220
Q8C550_MOUSE length AA
enriched library, clone:A230035L15 product:apoptosis
repressor with CARD domain [Nol3] [Mus musculus (Mouse)] align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
EPEPEPE D+
Sbjct: 202 EPEPEPEPDF 211

tr Q53YU5 Apoptosis repressor interacting with CARD (0 day neonate 220

Q53YU5_MOUSE eyeball
cDNA, RIKEN full-length enriched library,
clone:E130314L04 product:apoptosis repressor with CARD
domain) [Nol3] [Mus musculus (Mouse)]

AA
[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
EPEPEPE D+
Sbjct: 202 EPEPEPEPDF 211

tr Q73XH7 Fas [fas] [Mycobacterium paratuberculosis] 3092 AA
Q73XH7_MYCPA

[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
+PEPEPEAD
Sbjct: 1744 DPEPEPEAD 1752

tr Q478V8 Response regulator receiver:CheW-like protein:ATP- 1866
Q478V8_9RHO binding region, AA
ATPase-like:Hpt [Daro_3895] [Dechloromonas aromatica
RCB] [align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 831 EPEPEPEAE 839

tr Q9EXU1 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9EXU1_KLEPN

[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 3 VEPEPEPEAD 12
VEPEPEPE +
Sbjct: 42 VEPEPEPETE 51

tr Q6XXM0 Fatty acid synthetase I [fasI] [Mycobacterium] 3089

Q6XXM0_MYCSM smegmatis]

AA
alignScore = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)Query: 4 EPEPEPEAD 12
+PEPEPEAD
Sbjct: 1747 DPEPEPEAD 1755tr Q5MBX2 TonB2 [tonB2] [Actinobacillus suis] 281 AA
Q5MBX2_ACTSUalignScore = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 74 EPEPEPEAE 82tr Q4QZC1 Periplasmic energy transducer (Fragment) [tonB] 138
Q4QZC1_KLEPN [Klebsiella
pneumoniae] AAalignScore = 30.3 bits (64), Expect = 5.0
Identities = 8/10 (80%), Positives = 9/10 (90%)Query: 3 VEPEPEPEAD 12
VEPEPEPE +
Sbjct: 21 VEPEPEPETE 30tr Q9VAI5 CG15506-PB, isoform B [CG15506] [Drosophila melanogaster] 336
Q9VAI5_DROME (Fruit fly)] AAalignScore = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 321 EPEPEPEAE 329tr Q9N411 Prion-like-(Q/n-rich)-domain-bearing protein protein 82 300
Q9N411_CAEL [pqn-82] AA
[Caenorhabditis elegans]align

Score = 30.3 bits (64), Expect = 5.0

Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 2 SVEPEPEPEEA 11
SVE EPEPEEA
Sbjct: 244 SVEQEPEPEEA 253

tr Q8MZB6 AT15667p [CG15506] [Drosophila melanogaster (Fruit fly)] 297 AA
Q8MZB6_DROME

[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 282 EPEPEPEAE 290

tr Q8IMK6 CG15506-PA, isoform A [CG15506] [Drosophila melanogaster 297
Q8IMK6_DROME (Fruit fly)] AA
[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 282 EPEPEPEAE 290

tr Q4U8R9 Hypothetical protein [TA10045] [Theileria annulata] 599 AA
Q4U8R9_THEAN

[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 315 EPEPEPEAE 323

tr Q5AQG7 Hypothetical protein [AN9463.2] [Aspergillus nidulans 1737
Q5AQG7_EMENI FGSC A4] AA
[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12

EPEPEPEA+
Sbjct: 448 EPEPEPEAE 456

tr Q5ARPO Predicted protein [AN9040.2] [Aspergillus nidulans FGSC 179
Q5ARPO_EMENI A4] AA
[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 10/14 (71%), Positives = 10/14 (71%), Gaps = 4/14 (28%)

Query: 3 VEPEPE---PEAD 12
VEPEPE PEAD
Sbjct: 95 VEPEPEPEPAPEAD 108

tr Q5ATE5 Hypothetical protein [AN8435.2] [Aspergillus nidulans 850
Q5ATE5_EMENI FGSC A4] AA
[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 661 EPEPEPEAE 669

tr Q527B1 Hypothetical protein [MG06645.4] [Magnaporthe grisea 70- 717
Q527B1_MAGGR 15] AA
[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 356 EPEPEPEAE 364

tr Q526E4 Hypothetical protein [MG06862.4] [Magnaporthe grisea 70- 919
Q526E4_MAGGR 15] AA
[align](#)

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 466 EPEPEPEAE 474

tr Q4PFF2 Hypothetical protein [UM01161.1] [Ustilago maydis 521] 2649 AA
Q4PFF2_USTMA

align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 2312 EPEPEPEAE 2320

tr Q4IFF5 Hypothetical protein [FG04053.1] [Gibberella zeae PH-1] 807 AA
Q4IFF5_GIBZE

align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 5 PEPEPEADY 13
PEPEPE DY
Sbjct: 236 PEPEPEPDY 244

sp P26185 TonB protein [tonB] [Serratia marcescens] 247 AA
TONB_SERMA

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 75 VEPEPEPE 82

sp P25945 TonB protein [tonB] [Salmonella typhimurium] 242 AA
TONB_SALTY

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 69 VEPEPEPE 76

sp P45610 TonB protein [tonB] [Klebsiella pneumoniae] 243 AA
TONB_KLEPN

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
Sbjct: 68 VEPEPEPE 75

sp P46383 TonB protein [tonB] [Enterobacter aerogenes (Aerobacter 243 AA
TONB_ENTAE aerogenes)]

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
Sbjct: 69 VEPEPEPE 76

sp P02929 TonB protein [tonB] [Escherichia coli] 239 AA
TONB_ECOLI

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
Sbjct: 69 VEPEPEPE 76

sp Q62881 Nucleolar protein 3 [Nol3] [Rattus norvegicus (Rat)] 221 AA
NOL3_RAT

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
Sbjct: 179 VEPEPEPE 186

sp P97855 Ras-GTPase-activating protein binding protein 1 (GAP SH3- 465
G3BP_MOUSE domain AA
binding protein 1) (G3BP-1) (DNA helicase VIII)
(HDH-VIII) [G3bp] [Mus musculus (Mouse)] align

Score = 29.9 bits (63), Expect = 6.7

Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 191 VEPEPEPE 198

tr Q4SUQ6 Chromosome undetermined SCAF13844, whole genome shotgun 129
Q4SUQ6_TETNG sequence AA
[GSTENG00012352001] [Tetraodon nigroviridis (Green align
puffer)]

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 4 EPEPEPEAD 12
EPEPEPE D
Sbjct: 90 EPEPEPETD 98

tr Q62882 Hypothetical protein [Rattus norvegicus (Rat)] 139 AA
Q62882_RAT align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 97 VEPEPEPE 104

tr Q5NCU1 Ras-GTPase-activating protein SH3-domain binding protein 465 AA
Q5NCU1_MOUSE [RP23-336J1.4] [Mus musculus (Mouse)] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 191 VEPEPEPE 198

tr Q571F9 MKIAA4115 protein (Fragment) [G3bp] [Mus musculus 505
Q571F9_MOUSE (Mouse)] AA
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 231 VEPEPEPE 238

tr Q57P65 SsrAB activated gene [srfA] [Salmonella choleraesuis] 441 AA
Q57P65_SALCH [align](#)

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 169 VEPEPEPE 176

tr Q57NS2 Energy transducer; uptake of iron, cyanocobalamin; 281
Q57NS2_SALCH sensitivity to AA
phages, colicins [tonB] [Salmonella choleraesuis] [align](#)

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 110 VEPEPEPE 117

tr Q9S3M6 TonB protein (Siderophore-mediated iron transport 266
Q9S3M6_BORPE protein) [tonB] AA
[Bordetella pertussis] [align](#)

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 101 VEPEPEPE 108

tr Q8Z7E4 TonB protein [tonB] [Salmonella typhi] 242 AA
Q8Z7E4_SALTI [align](#)

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 69 VEPEPEPE 76

tr Q8XCC2 Energy transducer; uptake of iron, cyanocobalamin; 239
Q8XCC2_ECO57 sensitivity to AA
phages, colicins [tonB] [Escherichia coli O157:H7] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 69 VEPEPEPE 76

tr Q8FHW5 TonB protein [tonB] [Escherichia coli O6] 255 AA
Q8FHW5_ECOL6 align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 86 VEPEPEPE 93

tr Q885B3 Major facilitator family transporter [PSPT01922] 465
Q885B3_PSESM [Pseudomonas syringae pv. tomato] AA
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 422 VEPEPEPE 429

tr Q884X6 Flagellar assembly protein FliH, putative [PSPT01960] 272 AA
Q884X6_PSESM [Pseudomonas syringae pv. tomato] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 33 VEPEPEPE 40

tr	<u>Q83RM7</u>	Membrane protein, energy transducer [tonB] [Shigella	242
	Q83RM7_SHIFL	flexneri]	AA
			align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

```
Query: 3  VEPEPEPE 10
      VEPEPEPE
Sbjct: 72 VEPEPEPE 79
```

tr	<u>Q7WKX3</u>	Siderophore-mediated iron transport protein [tonB]	268
	Q7WKX3_BORBR	[<i>Bordetella</i>	AA
		<i>bronchiseptica</i> (<i>Alcaligenes bronchisepticus</i>)]	align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

```
Query: 3      VEPEPEPE 10
          VEPEPEPE
Sbjct: 103 VEPEPEPE 110
```

tr	<u>Q7W7I4</u>	Siderophore-mediated iron transport protein [tonB]	278
	Q7W7I4_BORPA	[Bordetella parapertussis]	AA align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

```
Query: 3      VEPEPEPE 10
          VEPEPEPE
Sbjct: 113 VEPEPEPE 120
```

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

```
Query: 3      VEPEPEPE 10
        VEPEPEPE
Sbjct: 103 VEPEPEPE 110
```

tr	<u>Q5PHV4</u>	Putative virulence effector protein [srfA] [Salmonella	399
	Q5PHV4_SALPA	paratyphi-a]	AA
			align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE

Sbjct: 127 VEPEPEPE 134

tr Q5PCS7 TonB protein [tonB] [Salmonella paratyphi-a] 242 AA
Q5PCS7_SALPA

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE

Sbjct: 69 VEPEPEPE 76

tr Q5NZS1 Translation initiation factor IF-2 [infB] [Azoarcus sp. 945
Q5NZS1_AZOSE (strain AA
EbN1)] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE

Sbjct: 159 VEPEPEPE 166

tr Q48GE4 Flagellar assembly protein FliH [fliH] [Pseudomonas 274
Q48GE4_PSESH syringae pv. AA
phaseolicola 1448A] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE

Sbjct: 33 VEPEPEPE 40

tr Q9ZG18 TonB [tonB] [Bordetella bronchiseptica (Alcaligenes 268 AA
Q9ZG18_BORBR bronchisepticus)]

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE

Sbjct: 103 VEPEPEPE 110

tr Q9S3Z9 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9S3Z9_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 42 VEPEPEPE 49

tr Q9S3Z7 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9S3Z7_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 42 VEPEPEPE 49

tr Q9S3Z6 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9S3Z6_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 42 VEPEPEPE 49

tr Q9R440 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9R440_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 42 VEPEPEPE 49

tr Q9R427 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9R427_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
Sbjct: 42 VEPEPEPE 49

tr Q9R426 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
 Q9R426_KLEPN
[align](#)

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
Sbjct: 42 VEPEPEPE 49

tr Q9EXU0 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
 Q9EXU0_KLEPN
[align](#)

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
Sbjct: 42 VEPEPEPE 49

tr Q9EXT9 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
 Q9EXT9_KLEPN
[align](#)

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
Sbjct: 42 VEPEPEPE 49

Database: EXPASY/UniProtKB

Posted date: Sep 12, 2005 12:34 PM

Number of letters in database: 758,486,757

Number of sequences in database: 2,312,053

Lambda	K	H
0.319	0.283	1.59

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

length of query: 13

length of database: 758,486,757

effective HSP length: 4

effective length of query: 9

effective length of database: 749,238,545

effective search space: 6743146905

effective search space used: 6743146905

T: 16

A: 40

X1: 16 (7.4 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 43 (21.6 bits)

S2: 62 (29.5 bits)

Wallclock time: 3 seconds

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[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Swiss-Prot](#)Search for

UniProtKB/TrEMBL

entry Q53H67

[Printer-friendly view](#)[Request update](#)[Q53H67](#)[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#)
[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	Q53H67_HUMAN
Primary accession number	Q53H67
Secondary accession numbers	None
Entered in TrEMBL in	Release 31, September 2005
Sequence was last modified in	Release 31, September 2005
Annotations were last modified in	Release 31, September 2005
Name and origin of the protein	
Protein name	Left-right determination, factor B preproprotein variant [Fragment]
Synonyms	None
Gene name	Name: LEFTY1
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

References

[1] NUCLEOTIDE SEQUENCE.

TISSUE=Colon;

Maruyama K., Sugano S.;

"Oligo-capping : a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides.";

Gene 138:171-174(1994).

[2] NUCLEOTIDE SEQUENCE.

TISSUE=Colon;

Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;

"Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library.";

Gene 200:149-156(1997).

[3] NUCLEOTIDE SEQUENCE.

TISSUE=Colon;

Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;

Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.

Comments

- **SIMILARITY:** Belongs to the TGF-beta family.

Cross-references

EMBL [AK222714](#); [BAD96434.1](#); -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

Ensembl ENSG00000143787; Homo sapiens. [Contig view]
 HGNC HGNC:6552; LEFTY1.
 CleanEx HGNC:6552; LEFTY1.
 GeneCards LEFTY1.
 GeneLynx LEFTY1; Homo sapiens.
 GenAtlas LEFTY1.
 GO GO:0008083; Molecular function: growth factor activity (*inferred from electronic annotation*).
 GO GO:0005160; Molecular function: transforming growth factor beta receptor binding (*inferred from electronic annotation*).
 GO GO:0016049; Biological process: cell growth (*inferred from electronic annotation*).
 QuickGo view.
 InterPro IPR001839; TGFb.
 IPR003942; TGFb4.
 IPR001111; TGFb_N.
 Graphical view of domain structure.
 Pfam PF00019; TGF_beta; 1.
 PF00688; TGFb_propeptide; 1.
 Pfam graphical view of domain structure.
 PRINTS PR01427; TGFBETA4.
 ProDom PD000357; TGFb; 1.
 [Domain structure / List of seq. sharing at least 1 domain]
 SMART SM00204; TGFB; 1.
 PROSITE PS00250; TGF_BETA_1; 1.
 HOVERGEN [Family / Alignment / Tree]
 ProtoMap Q53H67.
 PRESAGE Q53H67.
 ModBase Q53H67.
 SWISS-2DPAGE Get region on 2D PAGE.
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords**Growth factor.****Features**

Feature table viewer

Key	From	To	Length	Description
NON_TER	1	1		

Sequence information

Length: 366 AA [This is the length of the partial sequence]
 Molecular weight: 40826 Da [This is the MW of the partial sequence]

CRC64: A5AA26DE37658075 [This is a checksum on the sequence]

10 20 30 40 50 60

MQPLWLCWAL WVLPLASPGA ALTGEQLLGS LLRQLQLKEV PTLDRADMEE LVIPTHVRAQ

70 80 90 100 110 120
YVALLQQRSHG DRSRGKRFSQ SFREVAGRFL ASEASTHLLV FGMEQRLPPN SELVQAVLRL

130 140 150 160 170 180
FQEPVPKAAL HRHGRLSPRS AQARVTVEWL RVRDDGSNRT SLIDSRLVSV HESGWKAFDV

190 200 210 220 230 240
TEAVNFWQQL SRPRQPLLLQ VSVQREHLGP LASGAHKLVR FASQGAPAGL GEPQLELHTL

250 260 270 280 290 300
DLGDYGAQGD CDPEAPMTEG TRCCRQEMYI DLQGMKWAEN WVLEPPGFLA YECVGTCRQP

310 320 330 340 350 360
PEALAFKWPF LGPRQCIASE TDSLPMIVSI KEGGRTRPQV VSLPNMRVQK CSCASDGALV

PRRLQP

Q53H67 in FASTA
format

View entry in original UniProtKB/TrEMBL format

View entry in raw text format (no links)

Request for annotation of this UniProtKB/TrEMBL entry

BLAST BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-
MODEL



NPSA Sequence analysis
tools



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[view](#) selected as [InterPro View](#) 

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Identifier [TGFBETA4](#) [\[View Relations\]](#) [\[View Alignment\]](#)Accession [PR01427](#)No. of Motifs [14](#)Creation Date [01-NOV-2000](#)Title [Transforming growth factor beta 4 precursor signature](#)Database [PRINTS; PR01423](#) [TGFBETA](#)References [MIM; 601877](#)

Literature
References

1. KOTHAPALLI, R., BUYUKSAL, I., WU, S.-Q., CHEGINI, N. AND TABIBZADEH
Detection of ebaf, a novel human gene of the
transforming growth factor beta superfamily association of gene expression
with endometrial bleeding.
J.CLIN.INVEST. 99 2342-2350 (1997).

2. MENO, C., SAIJOH, Y., FUJII, H., IKEDA, M., YOKOYAMA, T., YOKOYAMA,
TOYODA, Y. AND HAMADA, H.
Left-right asymmetric expression of the TGF beta-family member lefty
mouse embryos.
NATURE 381 151-155 (1996).

Documentation

Abnormal endometrial bleeding is a common manifestation of gynaecological diseases. A human gene, termed endometrial bleeding associated factor, which is expressed strongly in endometrium, has been shown to be associated with abnormal endometrial bleeding [1]. The predicted protein product ebaf shares similarity with members of TGF-beta superfamily. Thus ebaf is a novel member of the TGF-beta superfamily and an endometrial tissue factor whose expression is associated with normal menstrual and abnormal endometrial bleeding [1].

Examples of lateral asymmetry are often found in vertebrates (e.g., the heart being on the left side), but the molecular mechanisms governing establishment of left-right (L-R) handedness are unknown [2]. It is now thought that the gene lefty, a member of the transforming growth factor family, may encode a morphogen for L-R determination [2]. Lefty protein which contains the cysteine-knot motif characteristic of this superfamily

is expressed in the left half of gastrulating mouse embryos. This asymmetry expression is transient and occurs just before the first sign of lateral asymmetry appears [2]. Thus lefty may be involved in establishing lateral asymmetry in the organ systems of mammals [2].

TGFBETA4 is a 14-element fingerprint that provides a signature for transforming growth factor beta 4 precursor proteins. The fingerprint was derived from an initial alignment of 2 sequences: the motifs were drawn from conserved regions spanning virtually the full alignment length, focusing on those sections that characterise TGF-beta 4 proteins but distinguish them from the rest of the TGF-beta superfamily. Two iterations on SPTR39_1 were required to reach convergence, at which point a true set comprising 4 sequences was identified. Several partial matches were also found (Q9W6I7, Q9PW55, Q9W6I6), all antiviral or Lefty proteins that match 2-4

Summary Information

4 codes involving 14 elements
0 codes involving 13 elements
0 codes involving 12 elements
0 codes involving 11 elements
0 codes involving 10 elements
0 codes involving 9 elements
0 codes involving 8 elements
0 codes involving 7 elements
0 codes involving 6 elements
0 codes involving 5 elements
1 codes involving 4 elements
1 codes involving 3 elements
2 codes involving 2 elements

Composite Feature Index

14	4	4	4	4	4	4	4	4	4	4	4	4	4	4
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	1	0	0	0	0	0	1	0	0	1	1	0	0
3	0	0	0	0	1	0	0	1	0	0	1	0	0	0
2	0	0	2	0	0	0	0	2	0	0	0	0	0	0
	1	2	3	4	5	6	7	8	9	10	11	12	13	14

True Positives	<u>075610</u>	<u>075611</u>	<u>TGF4_HUMAN</u>	<u>TGF4_MOUSE</u>
True Positive Partial	Codes involving 4 elements <u>Q9PVN4</u> Codes involving 3 elements <u>Q9W6I7</u> Codes involving 2 elements <u>Q9PW55</u> <u>Q9W6I6</u>			
Sequence Titles	<u>075610</u>	SIGNALING MOLECULE LEFTY-B - Homo sapiens (Human).		
	<u>075611</u>	SIGNALING MOLECULE LEFTY-A - Homo sapiens (Human).		
	<u>TGF4_HUMAN</u>	TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4)		
	<u>TGF4_MOUSE</u>	TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4)		
	<u>Q9PVN4</u>	LEFTY - Gallus gallus (Chicken).		
	<u>Q9W6I7</u>	SIGNALING MOLECULE LEFTY2 - Brachydanio rerio. (Zebrafish)		
	<u>Q9PW55</u>	ANTIVIN - Brachydanio rerio (Zebrafish) (Zebra danio).		
	<u>Q9W6I6</u>	SIGNALING MOLECULE LEFTY1 - Brachydanio rerio (Zebrafish)		
Scan History	SPTR39_14f 2 50 NSINGLE			
Initial Motifs	Motif 1 width=23			
	Element	Seqn Id	St	Int Rpt
	LWLCWALWVLPLAGPGAALTEEQ	TGF4_HUMAN	4	4 -
	LWLCWALWALSLSLREALTGEQ	TGF4_MOUSE	4	4 -
	Motif 2 width=22			
	Element	Seqn Id	St	Int Rpt
	QILGSLQLQLDQPPVLDKAD	TGF4_MOUSE	26	-1 -
	QLLASLLRQLQLSEVPVLDRAD	TGF4_HUMAN	26	-1 -
	Motif 3 width=17			
	Element	Seqn Id	St	Int Rpt
	EGMVIPSHVRTQYVALL	TGF4_MOUSE	49	1 -
	EKLVIPAHVRAQYVVLL	TGF4_HUMAN	49	1 -
	Motif 4 width=19			
	Element	Seqn Id	St	Int Rpt
	RSRGKRFSQNLREVAGRFL	TGF4_MOUSE	72	6 -
	RSRGKRFSQSFREVAGRFL	TGF4_HUMAN	71	5 -
	Motif 5 width=16			
	Element	Seqn Id	St	Int Rpt
	HLLVFGMEQRLPPNSE	TGF4_MOUSE	97	6 -
	HLLVFGMEQRLPPNSE	TGF4_HUMAN	96	6 -
	Motif 6 width=21			
	Element	Seqn Id	St	Int Rpt
	ELVQAVLRLFQEPVPQALHR	TGF4_HUMAN	111	-1 -
	ELVQAVLRLFQEPVPRTALRR	TGF4_MOUSE	112	-1 -
	Motif 7 width=19			
	Element	Seqn Id	St	Int Rpt
	RQKRLSPHSARARVTIEWL	TGF4_MOUSE	132	-1 -
	RHGRLSPAAPKARVTVEWL	TGF4_HUMAN	131	-1 -

Motif 8 width=22				
Element	Seqn Id	St	Int	Rpt
RDDGSNRTALIDSRLVSIHESG	TGF4_MOUSE	153	2	-
RDDGSNRTSLIDSRLVSVHESG	TGF4_HUMAN	151	1	-

Motif 9 width=24				
Element	Seqn Id	St	Int	Rpt
WQQLSRPRQPLLLQVSVQREHLGP	TGF4_MOUSE	187	12	-
WQQLSRPPEPLLVQVSVQREHLGP	TGF4_HUMAN	185	12	-

Motif 10 width=16				
Element	Seqn Id	St	Int	Rpt
HKLVRFAAQGTPDGKG	TGF4_MOUSE	216	5	-
HKLVRFASQGAPAGLG	TGF4_HUMAN	214	5	-

Motif 11 width=26				
Element	Seqn Id	St	Int	Rpt
QLELHTLDLKDYGAGNCDPEAPVTE	TGF4_MOUSE	236	4	-
QLELHTLDRDYGAGDCDPEAPMTE	TGF4_HUMAN	232	2	-

Motif 12 width=22				
Element	Seqn Id	St	Int	Rpt
RQEMYLDLQGMKWAENWILEPP	TGF4_MOUSE	267	5	-
RQEMYIDLQGMKWAENWVLEPP	TGF4_HUMAN	263	5	-

Motif 13 width=21				
Element	Seqn Id	St	Int	Rpt
QLPESLTSRWPFGLGPRQCVAS	TGF4_MOUSE	301	12	-
QPPEALAFNWPFLGPRQCIAS	TGF4_HUMAN	297	12	-

Motif 14 width=20				
Element	Seqn Id	St	Int	Rpt
PMIVSVKEGGRTRPQVVSLP	TGF4_MOUSE	327	5	-
PMIVSIKEGGRTRPQVVSLP	TGF4_HUMAN	323	5	-

Final Motifs

Motif 1 width=23				
Element	Seqn Id	St	Int	Rpt
LWLCWALWVLPLAGPGAALTEEQ	<u>TGF4_HUMAN</u>	4	4	-
LWLCWALWVLPLASPGAALTGEQ	<u>O75610</u>	4	4	-
LWLCWALWALSLSLREALTGEQ	<u>TGF4_MOUSE</u>	4	4	-
LWLCWALWVLPLAGPGAALTEEQ	<u>O75611</u>	4	4	-

Motif 2 width=22				
Element	Seqn Id	St	Int	Rpt
QILGSLLQQLQDQPPVLDKAD	<u>TGF4_MOUSE</u>	26	-1	-
QLLASLLRQLQLSEVPVLDKAD	<u>TGF4_HUMAN</u>	26	-1	-
QLLGSLLRQLQLKEVPTLDRAD	<u>O75610</u>	26	-1	-
QLLGSLLRQLQLSEVPVLDKAD	<u>O75611</u>	26	-1	-

Motif 3 width=17				
Element	Seqn Id	St	Int	Rpt
EGMVIPSHVRTQYVALL	<u>TGF4_MOUSE</u>	49	1	-
EKLVIPAHVRAQYVVLL	<u>TGF4_HUMAN</u>	49	1	-
EELVIPTHVRAQYVALL	<u>O75610</u>	49	1	-
EKLVIPAHVRAQYVVLL	<u>O75611</u>	49	1	-

Motif 4 width=19				
Element	Seqn Id	St	Int	Rpt

RSRGKRFSQNLREVAGRFL	<u>TGF4_MOUSE</u>	72	6	-
RSRGKRFSQSFRVAGRFL	<u>TGF4_HUMAN</u>	71	5	-
RSRGKRFSQSFRVAGRFL	<u>O75610</u>	72	6	-
RSRGKRFSQSFRVAGRFL	<u>O75611</u>	72	6	-
Motif 5 width=16				
Element	Seqn Id	St	Int	Rpt
HLLVFGMEQRLPPNSE	<u>TGF4_MOUSE</u>	97	6	-
HLLVFGMEQRLPPNSE	<u>TGF4_HUMAN</u>	96	6	-
HLLVFGMEQRLPPNSE	<u>O75611</u>	97	6	-
HLLVFGMEQRLPPNSE	<u>O75610</u>	97	6	-
Motif 6 width=21				
Element	Seqn Id	St	Int	Rpt
ELVQAVLRLRFQEPVPKAAALHR	<u>O75611</u>	112	-1	-
ELVQAVLRLRFQEPVPQALHR	<u>TGF4_HUMAN</u>	111	-1	-
ELVQAVLRLRFQEPVPKAAALHR	<u>O75610</u>	112	-1	-
ELVQAVLRLRFQEPVPRTALRR	<u>TGF4_MOUSE</u>	112	-1	-
Motif 7 width=19				
Element	Seqn Id	St	Int	Rpt
RQKRLSPHSARARVTIEWL	<u>TGF4_MOUSE</u>	132	-1	-
RHGRLSPAAPKARVTVEWL	<u>TGF4_HUMAN</u>	131	-1	-
RHGRLSPRSAQARVTVEWL	<u>O75611</u>	132	-1	-
RHGRLSPRSARARVTVEWL	<u>O75610</u>	132	-1	-
Motif 8 width=22				
Element	Seqn Id	St	Int	Rpt
RDDGSNRTALIDSRLVSIHESG	<u>TGF4_MOUSE</u>	153	2	-
RDDGSNRTSLIDSRLVSVHESG	<u>TGF4_HUMAN</u>	151	1	-
RDDGSNRTSLIDSRLVSVHESG	<u>O75610</u>	153	2	-
RDDGSNRTSLIDSRLVSVHESG	<u>O75611</u>	153	2	-
Motif 9 width=24				
Element	Seqn Id	St	Int	Rpt
WQQLSRPRQPLLLQVSVQREHLGP	<u>O75610</u>	187	12	-
WQQLSRPRQPLLLQVSVQREHLGP	<u>O75611</u>	187	12	-
WQQLSRPRQPLLLQVSVQREHLGP	<u>TGF4_MOUSE</u>	187	12	-
WQQLSRPPEPLLQVSVQREHLGP	<u>TGF4_HUMAN</u>	185	12	-
Motif 10 width=16				
Element	Seqn Id	St	Int	Rpt
HKLVRFASQGAPAGLG	<u>O75610</u>	216	5	-
HKLVRFASQGAPAGLG	<u>O75611</u>	216	5	-
HKLVRFAAQGTPDGKG	<u>TGF4_MOUSE</u>	216	5	-
HKLVRFASQGAPAGLG	<u>TGF4_HUMAN</u>	214	5	-
Motif 11 width=26				
Element	Seqn Id	St	Int	Rpt
QLELHTLDRDYGAQGDCDPEAPMTE	<u>O75611</u>	234	2	-
QLELHTLDLG DYGAQGDCDPEAPMTE	<u>O75610</u>	234	2	-
QLELHTLDLKDYGAGNCDPEAPVTE	<u>TGF4_MOUSE</u>	236	4	-
QLELHTLDRDYGAQGDCDPEAPMTE	<u>TGF4_HUMAN</u>	232	2	-
Motif 12 width=22				
Element	Seqn Id	St	Int	Rpt
RQEMYLDLQGMKWAENWVLEPP	<u>TGF4_MOUSE</u>	267	5	-
RQEMYIDLQGMKWAENWVLEPP	<u>TGF4_HUMAN</u>	263	5	-
RQEMYIDLQGMKWAENWVLEPP	<u>O75610</u>	265	5	-

RQEMYIDLQGMKWAKNWWLEPP

O75611

265

5

-

Motif 13 width=21

Element

QLPESLTSRWPFLGPRQCVAS

QPPEALAFNWPFLGPRQCIAS

QPPEALAFKWPFLGPRQCIAS

QPPEALAFNWPFLGPRQCIAS

Seqn Id

TGF4 MOUSE

TGF4 HUMAN

O75610

O75611

St

301

297

299

299

Int

12

12

12

12

Rpt

-

-

-

-

Motif 14 width=20

Element

PMIVSVKEGGTRPQVVSLP

PMIVSIKEGGTRPQVVSLP

PMIVSIKEGGTRPQVVSLP

PMIVSIKEGGTRPQVVSLP

Seqn Id

TGF4 MOUSE

TGF4 HUMAN

O75610

O75611

St

327

323

325

325

Int

5

5

5

5

Rpt

-

-

-

-

(data stored in EXT_LINK zone)

Hoverprot: TGFB4_MOUSE

ID TGFB4_MOUSE STANDARD; PRT; 368 AA.
AC Q64280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Transforming growth factor beta 4 precursor (TGF-beta 4) (Lefty
DE protein) (Lefty-1 protein) (STRA3 protein).
GN Name=Ebf; Synonyms=Lefty, Lefty1, Stra3, Tgfb4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96202359; PubMed=8610011; DOI=10.1038/381151a0;
RA Meno C., Saijoh Y., Fujii H., Ikeda M., Yokoyama T., Yokoyama M.,
RA Toyoda Y., Hamada H.;
RT "Left-right asymmetric expression of the TGF beta-family member lefty
RT in mouse embryos."
RL Nature 381:151-155(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Bouillet P.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98156497; PubMed=9496783;
RA Oulad-Abdelghani M., Chazaud C., Bouillet P., Mattei M.-G., Dolle P.,
RA Chambon P.;
RT "Stra3/lefty, a retinoic acid-inducible novel member of the
RT transforming growth factor-beta superfamily."
RL Int. J. Dev. Biol. 42:23-32(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Embryonic stem cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=98372436; PubMed=9708731; DOI=10.1016/S0092-8674(00)81472-5;
 RA Meno C., Shimono A., Saijoh Y., Yashiro K., Mochida K., Ohishi S.,
 RA Noji S., Kondoh H., Hamada H.;
 RT "Lefty-1 is required for left-right determination as a regulator of
 RT lefty-2 and nodal.";
 RL Cell 94:287-297(1998).
 CC -!- FUNCTION: Required for left-right axis determination as a
 CC regulator of LEFTY2 and NODAL.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DEVELOPMENTAL STAGE: By E8.0, expressed exclusively on the left
 CC side of developing embryos with expression predominantly in the
 CC prospective floor plate (PFP). Weak expression in the lateral-
 CC plate mesoderm (LPM).
 CC -!- PTM: The processing of the protein may also occur at the second R-
 CC X-X-R site located at AA 132-135. Processing appears to be
 CC regulated in a cell-type specific manner.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC -!- GENE_FAMILY: HBG074429 [FAMILY / ALN / TREE]
 DR EMBL; D83921; BAA12121.1; -; mRNA.
 DR EMBL; Z73151; CAA97497.1; -; mRNA.
 DR EMBL; AJ000082; CAA03909.1; -; mRNA.
 DR EMBL; AJ000083; CAA03910.1; -; Genomic_DNA.
 DR EMBL; BC050221; AAH50221.1; -; mRNA.
 DR PIR; S67507; S67507.
 DR HSSP; P10600; 1TGJ.
 DR Ensembl; ENSMUSG000000038793; Mus musculus.
 DR MGI; MGI:107405; Ebaf.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF_beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR01427; TGFbeta4.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR PRODOM; Q64280.
 DR SWISS-2DPAGE; Q64280.
 KW Cytokine; Developmental protein; Glycoprotein; Growth factor; Signal.
 FT DOMAIN 16 74 PRODOM:2002.1:PD037776 11
 FT DOMAIN 75 241 PRODOM:2002.1:PD583730 4
 FT DOMAIN 242 362 PRODOM:2002.1:PD328043 10
 FT SIGNAL 1 21 Potential.
 FT PROPEP 22 76 Or 135 (Potential).
 FT CHAIN 77 368 Transforming growth factor beta 4.
 FT CARBOHYD 158 158 N-linked (GlcNAc...) (Potential).
 FT DISULFID 253 266 By similarity.

FT DISULFID 265 318 By similarity.
FT DISULFID 295 353 By similarity.
FT DISULFID 299 355 By similarity.
SQ SEQUENCE 368 AA; 41498 MW; 821DAE663C546B5F CRC64;
MPFLWLCWAL WALSLVSLRE ALTGEQILGS LLQQQLQLDQP PVLDKADVEG MVIPSHVRTQ
YVALLQHSHA SRSRGKRFSQ NLREVAGRFL VSETSTHLLV FGMEQRLPPN SELVQAVLRL
FQEPVPR TAL RRQKRLSPHS ARARVTIEWL RFRDDGSNRT ALIDSRLVSI HESGWKAFDV
TEAVNFWQQL SRPRQPLLLQ VSVQREHLGP GTWSSSHKLVR FAAQGTPDGK GQGEPQLELH
TLDLKDYG AQ GNCDPEAPVT EGTRCCRQEM YLDLQGMKWA ENWILEPPGF LTYECVGSCL
QLPESLTSRW PFLGPRQCVA SEMTSLPMIV SVKEGGRTRP QVVSLPNMRV QTCSCASDGA
LIPRRLQP

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